Title: Perfect score: Sequence:

US-09-820-003B-1 1405 1 aagcgatagctgag

nucleic

nucleic search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

GenEmbl:*

1: gb_ba:*
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the number of results predicted by chance to

have

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

2054640 seqs, 14551402878 residues

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June 22, 2003, 18:57:03 ; Search time 3597 Seconds (without alignments)
11367.651 Million cell updates/sec
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1433) Strausberg, R. Direct Submission
                                                                                                                                                                                                                                                             BC000905 1433 bp mRNA linear PRI 12-JUL-2001 Homo sapiens, RAB1, member RAS oncogene family, clone MGC:5233 IMAGE:2900705, mRNA, complete cds. BC000905 BC000905 GI:14705268 MGC.
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AK055927 Homo sapi

BC002077 Mus muscu

AL050268 Homo sapi

AL050268 Homo sapi

Y00094 Mouse mRNA

AF226673 Mus muscu

AC123143 Rattus no

AC007318 Homo sapi

AL049545 Human DNA

AL512349 Homo sapi

X15747 Mouse ypti

X15747 Mouse ypti

AC117841 Rattus no

AC099548 Rattus no

AC099548 Rattus norv

X35384 Canine rabi

AC13807 Mus muscu

U63023 Rattus norv

X350384 Canine rabi

AC013807 Mus muscu

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X396159 Sequence

M28209 Homo sapi

AC1054411 Rattus no

AC196441 Rattus no

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AF227734 Felis cat

AC120626 Rattus norv

X38393 Discopyge o

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AC129645 Rattus no

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AC129647 Felis cat

AC129647 Felis Cat

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AC129647 Sarcophil

AF23738 Monodelph

AF398475 Homo sapi

AF398475 Elephas m

AF398477 Elephas m

AF398477 Elephas m
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Db 301 CAGCACANTTGGTGTGGATTTCAAAATAAAAAATACAATTACAACGATTACAACGATTACAACATTCAAAATACAATTCAAAATACAATTCAAAATACAATTCAAAATACAATTACAATTACAACTCAAATTCAAAAATTCAAAATTCAAAATTCAAAAAA		Qy 242 GGTTGGAAAGTCTTGCCTTCTTAGGTTTGCAGATACATATACAGAAAGCTACAT 301	QY 182 GTCCAGCATGAATCCCGAATATGATTATTTATTCAAGTTACTTCTGATTGGCGACTCAGG 241	QY 122 TCAGGGCGGCGGCAGCAAGGGCGGCGGCGGCGGCGGCAGCTGCAGTGACAT 181		Qy 3 GCGATAGCTGAGT-GCGGCGGCTGCTGATTGTGTTCTAGGGGACGAGTAGGGGAAGACG 61	Query Match 86.8%; Score 1219; DB 9; Length 1433; Best Local Similarity 93.2%; Pred. No. 2.8e-187; Matches 1336; Conservative 0; Mismatches 0; Indels 97; Gaps 2;	KQWLQEIDRYASENVNKLLVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATN VEQSFMTMAAEIKKENGPGATAGGAEKSNVKIQSTPVKQSGGGCC* BASE COUNT 432 a 254 c 326 g 421 t	/protein_id="AAH00905.1" /db_xref="GI:12654175" /translation="MSSMNPERDYLFKLLLIGDSGVGKSCLLLREADDTYTESYISTI /translation="MSSMNPERDYLFKLLLIGDSGVGKSCLLLREADDTYTESYISTI GVDEKIRTELDGKTTKLDIWDTAGOERFEFTTTSGYYRGAHGTTYVYDYFDORSFRNNY	<pre>/note="vector: pCMV-SPORT6" 179</pre>		rce	IRAK	information can l http://image.llnl	Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: villalon@bcm.tmc.edu. Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC	COntact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc.	REMARK NIH MGC Project URL: http://mgc.nci.nih.gov COMMENT On Jul 12, 2001 this sequence version replaced gi:12654174.	JOURNAL Submitted (16-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
	1286 1381	1321	1166	1106 1201	1046 1141	. 986 1081	926 1021	866 961	806 901	746 841	686 781	626 721	566 661	506 601	446 541	386 481	372 421	361	

1200 ATAGTTTCTTCATACTCTGCATATAATTTGTGGCTGCAGAATATTGTAATTTGTTGCACA	74 CGTTTGCTCCCGGAACAGCCTATCTCATTCCTTTCGATTACCCGTGGCGGGAG 133 120 AGTCAGGGCGGCGGCGCGCAGCAAGGGCGGCGGCGGCGGCGGC	ν _Q
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1020 GGCATGTTTAGATGTCAGGTTTAGTCTTGTAGGATGAAGTTCAGCCATTTTGTATCAAA 1079 	Qy Query Match 78.5%; Score 1103.6; DB 9; Length 2257; Best Local Similarity 92.4%; Pred. No. 1.2e-168; Matches 1233; Conservative 0; Mismatches 4; Indels 97; Gaps 2; Db	Query Best Matcl
960 CCTGATACCAGACTGTTTCCCGTGGTTAGGATATATATTTTGTTTTGATGTTTATATT 1019 	OUNT 669 a	BASE CO
900 AACTGTTTTAAACCTTTGTGTGCTGGTTTATAAAATAATGTGTGTAATCCTTGTTGCTTT 		
840 ATGGTCAATACTGACTTTTTTTTTATTCCCTTGACTCAAGACAGCTAACTTCATTTTCAG 	/clone_lib="NB9N41" Qy /note="cloning vector: pME18SFL3" Db CDS 194619 Db /note="unnamed protein product"	0
780 ACTGTATGTAGCTGCACTACAACAGATTCTTACCGTCTCCACAAAGGTCAGAGATTGTAA	/db_xref="taxon:9606"	
720 TCTCACAGCAATGAATTTGCAATCTGAACCCAAGTGAAAAAAAA	rce	FEATURES Sou
660 CAGAGCACTCCAGTCAAGCAGTCAGGTGGAGGTTGCTGCTAAAATTTGCCTCCATCCTTT	construction: Helix Research Institute (HRI) (supported by Japan Qy Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Blotechnology Center, National Institute of Technology and Db Evaluation; clone selection for full insert sequencing: RAB and	
600 AAAAAGCGAATGGGTCCCGGAGCAACAGCTGGTGGTGCTGAAAAGTCCAATGTTAAAATT 	(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library	COMMENT
540 ACCAGTGCTAAGAATGCAACGAATGTAGAACAGTCTTTCATGACGATGGCAGCTGAGATT		AUTH TITI JOUR
480 GTAGTAGACTACACAGCGAAGGAATTTGCTGATTCCCTTGGAATTCCGTTTTTGGAA 	Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T. TITLE NEDO human CDNA sequencing project JOURNAL Unpublished REFERENCE 2 (bases 1 to 2257)	TITI JOUR REFERE
420 GCCAGTGAAAATGTCAACAAATTGTTGGTAGGGAACAAATGTGATCTGACCACAAAGAAA 479 	Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Qy Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,	
360 AAGCTTCAAATAGAGTCCTTCAATAATGTTAAACAGTGGCTGCAGGAAATAGATCGTTAT 419	AUTHORS Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,	AUTH
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
300 ATCAGCACAATTGGTGTGGATTTCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATC	Clone_11b:NB9N41 clone:NB9N41000135. ORGANISM Homo sabiens ORGANISM Homo sabiens	ORGA
240 GGGGTTGGAAAGTCTTGCCTTCTTAGGTTTGCAGATGATACATATACAGAAAGCTAC 299 	ION AK055927 N AK055927.1 GI:16550777 DS cligo capping; fis (full insert sequence)	ACCESSIO VERSION KEYWORDS
180 ATGTCCAGCATGAATCCCGAATATGATTATTTATTCAAGTTACTTCTGATTGGCGACTCA 239 	ž	AK055927 LOCUS DEFINITIO
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Query Ma	BASE COUNT	CDS	FEATURES SOUTCE	REMARK COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	Db 1 QY 1 Db 1 QY 1 Db 1 QY 1 Db 1 Db 1 Db 1 DC02077 LOCUS DEFINITION
Match 74.9%; Score 1052.6; DB 10; Length 1444;	412	:3592802" tumor. Metallo rgin mouse. Ta aml" DRT6"	Contact: Dickson, I R. M. Clone dist through th Series: II This clone passed th	Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA MIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. Tissue Procurement: Gilbert Smith, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu	3	118 ATAGTTTCTTCATACTCTGCATATAAT? 260 CTATGTAACAAACAACTGAAGATATG?
Qy	Oy Db Oy Db	oy ob	0y 0y 0y 0y	D 04 D 04	D Q D Q D Q	Matc)
933 AATAATGTGTGTAATCCTTGTTGCTTCCTGATACCAGACTGTTTCCCGGTGGTTAG 992	866 TGAAAAAAATTGCCTGAATTGTACTGTATGTAGCTGCACTACAACAGATTCTTACC 925 814 GTCTCCACAAAGGTCAGAGATTGTAAATGGTCAATACTGAC-TTTTTTTTTATTCCCTTG 872	GTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCAGGTGGAGGTT	454 ACAAATGTGATCTGACCACAAGAAAGTAGTAGACTACACAACAGCGAAGGAATTTGCTG 513	370 TA	19 THANIC CHANTATHATTATICA AGTINCTIVE GALTEGATIC GALTEG	cal Similarity 88.3%; Pred. No. 1.9e-160; 1256; Conservative 0; Mismatches 59; Indels 108; Gaps 16 GCGGCGGCTGCTGATTGTGTTCTAGGGGACGGAGTAGGGGAAGACGTTTGCTCCCGGA

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                                                                                                                                Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKT2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKF2p564H163) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.blochem.mpg.de/proj/cDNA/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             Ammmalia; Eutheria; Primates; Catarrhini; Hominidae; Romo.

(bases 1 to 1208)

Wiemann, S., Well, B., Wellenreuther, R., Gassenhuber, J., Glassl, S., Ansorge, W., Boecher, M., Bloecker, H., Bauersachs, S., Blum, H., Lauber, J., Duesterhoeft, A., Beyer, A., Kochrer, K., Strack, N., Mewes, H.W., Ottenwaelder, B., Obermaier, B., Tampe, J., Heubner, D., Wambutt, R., Korn, B., Klein, M. and Poustka, A.

Toward a Catalog of Human Genes and Protetins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs Genome Res. 11 (3), 422-435 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1208 bp mRNA momo sapiens mRNA; cDNA DKFZp554B163 (from complete cds. AL050268
                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a,
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Wambutt,R., Heubner,D.,
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/organism-"Homo sapiens"
//db_xef-"taxon:9606"
//clone="DrFxp564B163"
/tissue_type="brain"
/clone_lib-"554 (synonym: hfbr2). Vector
X1-2blue; sies NotI + SalI"
/dev_stage="fetal"
191..580
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                                                                                                                                                                                                                                                                                                                                  Mewes, H.W., Gassenhuber, J. and Wiemann,
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clone DKFZp564B163);
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            TCTCACAGCAATGAATTTGCAATCTGAACCCAAGTGAAAAAACAAAATTGCCTGAATTGT
                                TCTCACAGCAATGAATTTGCAATCTGAACCCAAGTGAAAAAACAAAATTGCCTGAATTGT 779
                                                                       CAGAGCACTCCAGTCAAGCAGTCAGGTGGAGGTTGCTGCTAAAATTTGCCTCCATCCTTT
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ilarity 90:0%;
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191. 1580
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Haubruck,H., Disela,C., Wagner,P. and Gallwitz,
The ras-related ypt1 protein is an ubiquitous e
isolation and sequence analysis of mouse cDNA c
homologous to the yeast YPT1 gene
EMBO J. 6 (1987) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                         Submitted (13-NOV-1987) Gallwitz D., Max-Planck-Institut fuer biophysikalische Chemie, Abt. Molekulare Genetik, Postfach 2841,
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 1428)
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                                                                                                                                                                                                                                                                                                                                                                 Gallwitz, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
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                                                        /organism="Mus musculus"
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895 TTCAGAACTGTTTTAAACCTTTGTGTGCTGGTTTATAAATAA	Qy 656 AATTCAGAGCACTCCAGTCAAGCAGTCAGGTGGAGGTTGCTGCATAAATTTGCCTCCATC 715	Qy 476 GANAGTAGTAGACTACACAGAGGAAGATTTCCCTGTTTTT 33 Qy 476 GANAGTAGTAGACTACACAGAGGAAGTTCCCTTGGAATTCCCTTTGGAATTCCCTTTTT 480 Db 421 GANAGTAGTAGACTACACAGCAGCAGATTTAGCAGATTCCCTTGGAATTCCATTTTT 480 Qy 536 GGANACCAGTGCTAAGAATGCAACGAATGTAGAACAGTCTTTCATGACGATGGCAGCTGA 595	AAGATI TGATGI TTATGC	ORIGIN OUETY Match OUETY Match Best Local Similarity 88.5%; Pred. No. 1.1e-144; Best Local Similarity 88.5%; Pred. No. 1.1e-144; Matches 1123; Conservative 0; Mismatches 45; Indels 101; Gaps 4; Matches 1123; Conservative 0; Mismatches 45; Indels 101; Gaps 4; Ouety Matches 1123; Conservative 0; Mismatches 45; Indels 101; Gaps 4; Ouethes 1123; Conservative 0; Mismatches 45; Indels 101; Gaps 4; Ouethes 1123; Conservative 0; Mismatches 45; Indels 101; Gaps 4; Ouethes 1123; Conservative 0; Mismatches 45; Indels 101; Gaps 4; Ouethes 1123; Conservative 0; Mismatches 45; Indels 101; Gaps 4; Ouethes 1123; Conservative 0; Mismatches 45; Indels 101; Gaps 4; Ouethes 1123; Conservative 0; Mismatches 45; Indels 101; I

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REFERENCE
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Davila, M.I. Davis, C. Davy, Corroll, L. Dederich, D.A. Davis, C. Davis, C. Davy, Carroll, L. Dederich, D.A. Davis, C. Davis, C. Davy, Carroll, L. Dederich, D.A. Douthwaite, K.J. Draper, H. Dugan-Rocha, S. Durbin, K.J. Earnhart, C. Edgar, D. Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C. Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hatt, M., Havlak, P., Hawes, A., Hernandez, J., Honsi, F., Howard, S., Huber, J., Hulk, S., Hume, J., Joddah, S., Karlsson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Meris, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Nguyen, N., Nickerson, E., Novenkov, S., Oguh, M., Okwuonu, G., Oragunye, N., Ovledo, R., Pace, A., Payton, B., Peery, J., Perez, L., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Soott, G., Shen, H., Shooshtari, N., Sisson, I., Sutton, A., Vasquez, L., Vara, V., Villalon, D., Vinson, R., Wang, O., Wang, O., Warren, R., Washington, C., Watlington, S., Wang, O., Warren, R., Washington, C., Watlington, S., Wang, O., Warren, R., Washington, C., Watlington, S.,
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***, 50 unordered pieces.
AC123143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bryant, N.P.,
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Worley, K.C.

Direct Submission

Direct Submission

Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030 Teplaced g1:21239895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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                                                        (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jul 4, 2002 this sequence version replaced g1:21239895
------ Genome Center
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 151988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 108541 bases at least Q40
Consensus quality: 113010 bases at least Q30
Consensus quality: 115635 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: GMGF
Center clone name: CH230-247B24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
1041: contig of 1041 bp in length 1141: gap of unknown length
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	624 ACAGCTGGTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCA 683 [504 GAATTTGCTGATTCCCTTGGAATTCCGTTTTTGGAAACCAGTGCTAAGAATGCAACGAAT 563		76346 TACAGAGGAAGCCATGTTATCATAGTTGTGTATGATGTGACCGACC	360 AAGCTTCAAATA	300 ATCAGCACAATTGGTGTGGATTTCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATC 359 	100 ATGTCCAGCATGATICC CGAPTATIGATITATICAGGTTACTICTIGATITGGGGACTCA 239	AGTCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		Query Match 58.4%; Score 820.6; DB 2; Length 151988; Best Local Similarity 78.8%; Pred. No. 5.8e-123; Matches 1196; Conservative 0; Mismatches 114; Indels 207; Gaps 10; 1 AAGCGATAGCTGAGT-GCGGGGGTGCTGATTGTGTTTCTAGGGGACGAGTAGGGAAGA 59	/db_xref="taxon:10116" /clone="cH230-247B24" /4145 a 28740 c 28161 g 43504 t 7438 others

21210 21309 gap of unknown lengt 23181 23282 gap of unknown lengt 23183 23282 gap of unknown lengt 23283 24419 gap of unknown lengt 24420 26447 gap of unknown lengt 24648 28422 contig of 2128 bp it 26442 agap 2522 gap of unknown lengt 24420 30850 contig of 1735 bp it 24420 30851 30950 gap of unknown lengt 24423 30850 contig of 2328 bp it 30951 3274 32773 contig of 1823 bp it 35271 35370 gap of unknown lengt 3274 32873 gap of unknown lengt 34842 34828 contig of 1829 bp it 35271 35370 gap of unknown lengt 44920 44919 contig of 2887 bp it 34920 44919 contig of 2887 bp it 34920 45019 gap of unknown lengt 44920 45019 gap of unknown lengt 45028 50253 gap of unknown lengt 50254 5323 contig of 2897 bp it 50254 5323 gap of unknown lengt 50256 contig of 3401 bp it 60265 6325 6325 bp of unknown lengt 63245 pp of unknown lengt 63246 gap of unknown lengt

FEATURES source

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Direct Submission
Submitted (23-MAR-2001) Genome
University School of Medicine,
                                                    Waterston, R.H.
                                                                                   Direct Submission
Submitted (16-APR-1999) Genome
University School of Medicine,
MO 63108, USA
                                                                                                                                                                                   The sequence of Homo sapiens 
Unpublished
                                                                                                                                                                                                                   2 (bases 1 to 204230) Wollam, A., Hawkins, M.,
                                                                                                                                                                                                                                                                                  1 (bases 1 to 204230)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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AC007318.4 GI:1:
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                                                                  (bases 1 to 204230)
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clone RP11-420C9
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Primates;
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apiens BAC clone
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                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Sequencing Center, Washin 4444 Forest Park Parkway,
                                                                                                  Sequencing Center, Washington 4444 Forest Park Parkway, St.
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5 (bases
                                                                                                           Direct Submission
Submitted (07-0002) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
On Mar 23, 2001 this sequence version replaced (
                                                                                                                                                                             Waterston, R.
                                                                                                                                                                                          University, 4444 Forest 6 (bases 1 to 204230)
                                                                                                                                                                                                                      Submitted (09-AUG-2001)
                                                                                                                                                                                                                                       Direct
                                                                                                                                                                                                                                                         Waterston, R.
                                                                                                                                                                                                                                                                        (bases
             Web site: http://genome.wustl.edu.
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NH0420C09
                                                              Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                       Submission
                                                                                                                                                                                                                                                                                       USA
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                                                                                               --- Genome Center
                                                                                                                                                                                                                                                                        204230)
                                                                                                                                                                                                         Department of Genetics, Park Avenue, St. Louis,
                                                                               Sequencing
                                                                                                             g1:7630984.
                                                                                                                           Washington
Missouri 63108,
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Missouri 6
                                                                                Center
                                                                                                                                                                                                         63108,
                                                                                                                             USA
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clone. sections It may be shorter because we only sequence overlapping sections once, or longer because we provide a small over n neighboring data submissions. This sequence may not represent the entire insert of this small overlap

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. I MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc D.

MAPPING INFORMATION:

SOURCE INFORMATION:

The RPCI:11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-350H15; the clone sequenced to the right is Actual start of this clone is at base to the right is AC034121. Actual end is at base position 1 of RP11-420C9; actual end is at base position 204230 of position 1 RP11-420C9. pBACe3 of this clone is at base at base position 204230

The sequence n... of PCR product from clone DNA. of PCR product from clone DNA. represents sequence of a single annilification of clone DNA. sequence RP11-420C9 from base position 44230 to 46506 consists ${}^2\mathrm{CR}$ product from clone DNA. Base position 44700 to 44774 Base position 44' plasmid subclone derived from PCR

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FEATURES
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890. .1082
/rpt_family="MER1_type" 1498. .1789
                                                          /clone="RP11-420C9"
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179. .486
                                                                                                        /map="2"
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/db_xref="taxon:9606"
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Oy 982 TGGTTGGTTAQAARTATTTTGTTTTATATTTGCATGTTTAQATGTCAGGTTT 1041	802 CAGATTCTTACCGTCTCCACAAAGGTCAGAGATTGTAAATGGTCAATACTGACTTTTTTT	Qy 622 CARCAGCTGGTGGTCGTGAGAACTCCAATGTTAAAATTCAGAGCACTCCAACCAGT 681	502 AGGAATTTGCTGATTCCCTTGGAATTCCGTTTTTGGAAACCAGTGCTAAGAATGCAACGA 56	8251 8251 8251 8251 8261 827 827 8281 8281 8281 8281 8281 8281	misc_feature

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         562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enguiries: humquery@sanger.ac.uk Clone requests: clonerequestssanger.ac.uk on May 14, 2002 this sequence version replaced gi:19068263. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-19L22 from the RPCI-23 Mouse PAC Library constructed by the group of Pleter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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/db_xref="taxon:10090"
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                               Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestdsanger.ac.uk
On Feb 23, 2001 this sequence version replaced gi:12956981.
                                                                                                                                                                                                                                                                                            116614 bp
Homo sapiens chromosome 6 clone
PROGRESS ***, in ordered nicona
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Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL

This sequence is the entire insert of clone 26377. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Jun 7, 1999 this sequence version replaced gi:4835284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requests: clonerequest@sanger.ac.uk
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Mammalia; Eutheria; Primates;
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ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 6, constructed by the Sanger Centre Chromosome 19 Group. Further information can be found at //www.sanger.ac.uk/HGP/Chr6
1s from the library RPCII constructed at the Roswell Park institute by the group of Pleter de Jong. For further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute by the group of Pieter de Jong. Ros see http://bacpac.med.buffalo.edu/ VECTOR:
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/note="dJ263J7.1 (RPL7 (60S Ribosomal Protein L7)
/note="dJ263J7.1 (RPL7 (60S Ribosomal Protein L7)
pseudogene); match: cDNAs: Em:X52967 Em:X57959 Em:L16558
Em:X57958 Em:M85235 Em:M17422 Em:M9016 Em:X57961
Em:X57950 Em:U63785; match: ESTs: Em:AL047212 Em:AI683841
Em:X57950 Em:U63785; match: ESTs: Em:AA047212 Em:AI683841
Em:AL609411 Em:AL620251 Em:AL678713 Em:AA853290
Em:AI188448 Em:AI1246632 Em:F29697.1 Em:AA640941
Em:AA147085 Em:AI354542 Em:AA648558 Em:AA172041
                                                                                                                                                                                                                                        complement(11030.
                                                                                                                                                                                                                                                                                             /note="LIP repeat: matches 1712. .3049 of consensus"
complement(11030. .11749)
/gene="dJ263J7.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'organism="Homo sapiens"
                                                                                                                                                                                                                                 'gene="dJ263J7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1PA12 repeat: matches 4282. .6165 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluYb8 repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "MLT1J repeat: matches 36. .174 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L1P5 repeat: matches -237. .5623 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIPS repeat: matches -1405. .-405 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 3049.
                                                                                                                                                                                                                                                               .11749)
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                                                                                                                                                                                                                                                                                                                                                                                                                            .317 of consensus"
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Em:AA093750; match:
Sw:P05426 Sw:Q42208
Sw:P11874 Sw:P32100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="LlPA13 repeat: matches 647. .1730 of 12908. .13190
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11790. .12860
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11307. .11789
                                                                                                                                                        'note="L1MA2 repeat:
                                                                                                                                                                                                                                                                                                  note="AluSx repeat: matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1PB3 repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L1PB3 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note-"L1PBa repeat: matches -1549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L1P repeat: matches 638. .4389 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="L1PA4 repeat: matches 5413. .6144 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                      note="L1MA2 repeat: matches 2533. .6308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                   note="MIR repeat: matches 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                    e="match: EST AA528504"
                                                                                                                                                                                                                                                                              e="MIR repeat: matches 8.
                                                                                                                                          .41630
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                                                                                                                                                                                               repeat: matches 3, .305 of consensus"
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                                     repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 6081.
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Sw:O01802 Sw:O60143 Sw:P25457
Sw:P05737 Sw:Q12213 Tr:O14371
                                       matches
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O2 Em:AA608110 'Em:AA745100

L3 Em:AA314838 Em:AA736534

D8:Em:W77465 Em:AA648073 Em:AA648202

O2 Em:U51697 Em:D51979 Em:D52053

A Em:N98334 Em:AA649499 Em:AA879164

B8 Em:AA173529 Em:AA091272
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Em: AA313220
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                                       .79 of consensus"
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  .466
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                                                                                                                   .2698 of consensus"
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AC067945/c
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Isak,A., Elliott,G., Doebber,A., Abbott,A., Hawkins,M. and Falk,A.
The sequence of Homo sapiens BAC clone RP11-629B4
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                         Waterston,R.

Direct Submission
Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 on Apr 25, 2001 this sequence version replaced gi:13518285
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (09-AUG-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 162471)
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5 (bases 1 to
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Submitted (25-APR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 6310B, USA
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Direct Submiss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162471 bp DNA Homo sapiens BAC clone RP11-629B4 from AC067945
                                                                                   This sequence was finished as follows unless otherwise noted:
                                                                                                                              between neighboring data submissions.
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                                                                                                                                           OTICE: This sequence may not represent the entire insert of this lone. It may be shorter because we only sequence overlapping lone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATAGACAACCAACAAAATGGAAGAAAA 94370
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                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                             Contact: sapiens@watson.wustl.edu
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    Genome Center

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from more than one subclone; and the assembly was confirmed γď

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. I MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Louis

SOURCE INFORMATION:

Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute Tateno, M., Ca approach for VECTOR: (http://bacpac.med.buffalo.edu) ibraries. RPCI-11 CI-11 human BAC library was made from the blood of one male as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., A., Catanese, J.J. and de Jong, P.J. (1988) An improved ch for construction of bacterial artificial chromosome cles. Genomics 51:1-8. The clone may be obtained either from the construction of the clone may be obtained either from the construction of the clone may be obtained either from the construction of the clone may be obtained either from the construction. pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-45219, 200 bp overlap; the clone sequenced to the right is RP11-317J9. Actual start of this clone sequenced to the right is RP11-629B4; actual end is at base position 195 of RP11-629B4; actual end is at base position 162471 of RP11-629B4.

Location/Qualifiers

/rpt_famil 5997. .613 /rpt_family="L1" 5108. .5242 /rpt_family="Alu" 4776. .5044 /rpt_family="Alu" 6135. .6178 /rpt_family="MIR' 4158. .4475 rpt_family="MIR" rpt_family="AT_rich" rpt_family="Alu" 'clone_lib="RPCI-11" /clone="RP11-629B4" 'chromosome="2" /organism="Homo sapiens" /db_xref="taxon:9606" rpt_family-"AT_rich" rpt_family="Alu" _family="L1" . 5465 . 2071 y="Alu"

/rpt_ 12297

_family="(TTTTG)n"

_family-

"AT_rich"

/rpt_ 10528. .10562

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_family="AT_rich" family-"AT_rich"

rpt_family="Alu"

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YY 1 AAGCGATAGCTGAGT-GGGGGGCTGCTGATTGTGTTCTAGGGGGACGGATAGGGGGAAGA 59	Query Match 48.7%; Score 684.4; DB 9; Length 162471; Best Local Similarity 71.1%; Pred. No. 5.4e-101; Matches 1337; Conservative 0; Mismatches 76; Indels 427; Gaps	repeat_region 47840 48153	<pre>repeat_region 47727 47789</pre>			/rpt_fam 42719.	/rpt_fa 42641.	/rpt_fa 42371.	_icgion	region 37354	region 36502	/rpt_fa	region lipt_fa	repeat_region 28065. 28896 /rpt_family="Alu" repeat_region 28881 .28841	/rpt_fa	_region		/rpt_ 26754	repeat_region 25927. 26475 /rpt_fam1ly="L2" repeat_region 26500. 26664	repeat_region 25554. 25846 /rpt_family="Alu"		repeat_region 22866 22860 /rpt_family="CT-rich"	repeat_region 21523. 2118" /rot family="blu"	/rpt_family="AT_rich" repeat_region 21212 .21327	<pre>/rpt_family="L2" repeat_region 20271 20291</pre>	_		repeat_region 18139. 18209 /ret_family="L2" repeat region 1871 1871	 	repeat_region 17221. 17290
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Submitted (07-JUL-1989) Wichmann H., MPI of Biophysical Chemi
Dept of Molecular Genetics, P O Box 2841, D-3400 Goettingen,
2 (bases 1 to 4678)
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 4678)
                                                                                                                                                                                                                                                       Mouse ypt1 gene for ras-related GTP-binding protein, X15747
X15747.1 GI:55463
GTP-binding protein; ras-related protein; ypt1 gene.
                                                                                                                                                                                                                                      Mus musculus
                                                                                                                  Wichmann, H., Disela, C., Hau
Nucleotide sequence of the
GTP-binding protein
                                                                                                                                                                                              Wichmann, H.
                                                                                                                                                                                                                                                Mus musculus.
                                                                                                        Nucleic Acids Res. 17 (16), 6737-6738 (1989)
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/organism="Mus musculus"
/strain="c(CH)/c(CH)"
/db_xref="taxon:10090"
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2519 CATATAATTTGTGGCTGCAGAATATTGT-ATTTGTTGCACACTATGTAACAA---AACTG 2574
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AC117841.4 GI:21746140
HTG; HTGS_PHASE1.
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****** 3 unordered pieces.
Submitted (11-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                            Worley, K.C.
Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                               Direct Submission
                                                     Unpublished
2 (bases 1 to 207945)
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5, *** SEQUENCING IN PROGRESS
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Submitted (17-7UL-2002) Human Genome Sequencing Center, Department Submitted (17-7UL-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20258099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 207945)
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NOTE: This is a 'working draft' sequence. It currently consists of 73 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center Clone name: CH230-360/6
Center Clone name: CH230-360/6
Center Clone name: CH230-360/6
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 139582 bases at least Q30
Consensus quality: 1349682 bases at least Q30
Consensus quality: 138682 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine Center code: BCM
Center bcm. The code: Context: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
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REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 14 AC117841/c LOCUS

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Rattus norvegicus clone CH230-901,
67 unordered pieces.
AC099354
                                                                                 Direct Submission
Submitted (10-NOY-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 174028)
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Muzny,D.M., Adams,C., Adio-Oduola
Alsbrooks,S.L., Amaratunge,H.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: GDIS
Center clone name: GDIS
Center clone name: GTS-10-901
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 127332 bases at least Q30
Consensus quality: 131924 bases at least Q30
Consensus quality: 131924 bases at least Q20
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 67 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.o
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Search completed: June 22, 2003, 20:54:20 Job time : 3615 secs	Qy 1 AAGCGATAGCTGAGT-GCGGCGGCTGCTGATTGTGTTCTAGGGGACGGAGTAGGGGAAGA 59
Oy 923 TGCTTTATA 931 Db . 99703 TGCTTTGTA 99695	Query Match 40.8%; Score 573.8; DB 2; Length 174028; Best Local Similarity 79.9%; Pred. No. 3.7e-83; Matches 822; Conservative 0; Mismatches 97; Indels 110; Gaps 8;
OY 863 TATTCCCTTGACTCAAGACAGCTAACTTCATTTTCAGAACTGTTTTAAACCTTTGTGTGC 922	111140: gap of unknown length 114378: contig of 3238 bp in 114478: gap of unknown length 1147845: contig of 3367 bp in
QY 804 GATTCTTACCGTCTCCACAAAGGTCAGAGATTGTAAATGGTCAATACTGACTTTT-TTTT 862	gap of unknown length contig of 3514 bp in gap of unknown length contig of 3271 bp in
QY 744 TGAACCCAAGTGAAAAACAAAATTGCCTGAATTGTACTGTATGTA	98212: gap of unknown length 100745: contig of 2533 bp in 100845: gap of unknown length 104055: contig of 3210 bp in
QY 684 GGTGGAGGTTGCTGCTAAAATTTGCCTCCATCCTTTTCTCACAGGAATGAAT	91899: gap of unknown length 95211: contig of 3312 bp in 95311: gap of unknown length 98112: contig of 2801 bp in
QY 624 ACAGCTGGTGGTGGTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCA 683	82952: gap of unknown length 86851: contig of 3899 bp in 86951: gap of unknown length 91799: contig of 4848 bp in
QY 564 GTAGAACAGTCTTTCATGACGATGGCAGCTGAGATTAAAAAGCGAATGGGTCCCGGAGCA 623	77262: gap of unknown length 80487: contig of 3225 bp in 80587: gap of unknown length 82852: contig of 2265 bp in
QY 504 GAATTIGCTGATICCCTIGGAATTCCGTTTTTGGAAACCAGTGCTAAGAATGCAACGAAT 563 	gap of unknown length contig of 2730 bp in gap of unknown length contig of 3615 bp in
QY 444 TIGGTAGGGAACAAAIGTGATCTGACCACAAAGAAAGTAGTAGACTACAACAACAGCGAAG 503	65056: gap of unknown length 67731: contig of 2675 bp in 67831: gap of unknown length 70617: contig of 2786 bp in
QY 384 AATGTTAAACAGTGGCTGCAGGAAATAGATCGTTATGCCAGTGAAAATGTCAACAAATTG 443	61037: gap of unknown length 63206: contig of 2169 bp in 63306: gap of unknown length 64956: contig of 1650 bp in
QY 372	57612: gap of unknown length 59522: contig of 1910 bp in 59522: gap of unknown length 60937: contig of 1315 bp in
Qy 360 AAGCTTCAAATA	54223: gap of unknown length 55763: contig of 1540 bp in 55863: gap of unknown length 57512: contig of 1649 bp in
QY 300 ATCAGCACAATIGGTGTGGATITCAAAATAAGAACTATAGAGGTTAGACGGGAAAACAATC 359 	49010: gap of unknown length 51895: contig of 2885 bp in 51995: gap of unknown length 54123: contig of 2128 bp in
QY 240 GGGGTTGGAAAGTCTTGCCTTCTTGGTTTTGCAGATGATACATATACAGAAAGCTAC 299	gap of unknown length contig of 2557 bp in gap of unknown length contig of 2840 bp in
QY 180 ATGTCCAGCATGAATCCCGAATATGATTATTTATTCAAGTTACTTCTGATTGGCGACTCA 239	38955: gap of unknown length 40675: contig of 1720 bp in 40775: gap of unknown length 43313: contig of 2538 bp in
QY 120 AGTCAGGGCGGCGGCGGCAGCAAGGGGGGGGGGGGGGGG	34833: gap of unknown length 36561: contig of 1728 bp in 36661: gap of unknown length 38855: contig of 2194 bp in
QY 60 CGTTTGCTCTCCCGGAACAGCCTATCCTCATTCCTTTCGATTACCCGTGGCGCGGAG 119	31865: 32886: 32986: 34733:

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Title:
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                                                                                                                      26-MAR-1999;
17-DEC-1999;
                                                                                                                                                                                                                                     05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC60009;
                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                       22-MAR-2000; 2000WO-US07535.
                                                                                                                                                                                                                                                                                   WO200058356-A1.
                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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21	22	23	20	20	16	24	22	22	22	22	22	22	22	22	22	21	23	22	22	21	20	22	20	23	22	22	24	23	23	23	21	24	22	22	22
AAC35200	AAH87926	ABL05983	AAX23476	AAX23507	AAT19274	ABS14299	AAI06747	AAI46285	AAI21030	AAK40268	AAK14525	ABA33177	ABA66102	ABA48222	AAS34668	AAA42979	AAS83862	AAI93456	AAS44924	AAF21661	AAX27232	AAH55559	AAV88033	ABV04892	AAF17849	AAS47279	ABL75210	ABV44007	ABV35165	ABV14061	AAC06621	ABS01772	AAI01752 ·	AAI33136	AAI11818
thali	Peppermint plant o	phila melano	neutrophil	_	_	genome	#6738	#14971 used		bone m	brain e	#11643	foetal			Human secreted exp	DNA encoding novel	Human polynucleoti	æ	Human breast and o		Human breast tumou	\vdash	prostat	breast	_	tassel-de:	prostate	prostate	prostate	_	genome-deri	#17.43 used	#1822	for

Human secreted protein gene 44 SEQ ID NO:54.

Human; secreted protein; diagnosis; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antializer(c; hepatotropic; antidiabetic; antinflammatory; antiulocr; vulnerary; anticonvulsant, antibucterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; wound healing; neurological disease; infectious disease; chromosome identification;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC and cells the genes are expressed in Examples of activities include:
CC cytostatic; immunosuppressive; nootropic; antiinfammatory; antiviral;
CC antiallergic; hepatotropic; antibacterial; antifungal; antiviral;
CC vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; and
CC preventing, treating or ameliorating a medical condition in e.g. humans,
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The
CC increase or decrease storage capabilities. The polynucleotides are
CC increase or decrease storage capabilities. The polynucleotides are
CC diagnosing a disorder related to the female reproductive system,
CC diagnosing a disorder related to the female reproductive system,
CC particularly breast and/or ovary cancer. Whey are also useful in the gene
CC therapy of breast and ovarian cancer. Nucleic acids, protein, antibodies,
CC agonists and antagonists from the present invention are useful in the
CC diagnosis, treatment and prevention of cancer, immune disorders,
CC cardiovascular disorders, wound healing, neurological diseases and
CC used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 1319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB34852 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the presen invention. Human secreted proteins have activities based on the tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorder cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotide sequences given in AAC59966 to AAC60015 encode the necreted proteins given in AAB34773 to AAB34822. AAB34823 to
                384
                                      448
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)B; AAB34816.
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  AATGTTAAACAGTGGCTGCAGGAAATAGATCGTTATGCCAGTGAAAATGTCAACAAATTG
                                                                                                                                      ATCAGCACAATTGGTGTGGGATTTCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATC
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                                      TACAGAGGAGCCCATGGCATCATAGTTGTGTATGATGACAGATCAGGAGTCCTTCAAT
                                                                                                               AAGCTTCAAATA--
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92.9%;
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Pred. No. 4.4e-155;
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TCCATGCATAAAGTTTAGTGAGATGTTATATGTAAGATCTGATTTGCTAGTTCTTCCTTG
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AATTTGTGGCTGCAGAATATTGTAATTTGTTGCACACTATGTAACAAAACAACTGAAGAT
                                                                                                                       TAGAGTTATAAATGGAAAGATTACACTATCTGATTAATAGTTTCTTCATACTCTGCATAT
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CC Supecification, but was obtained in electronic format directly from WIPO control of the control of the printed control of the control of the printed control of the control of the control of the printed control of the control of the control of the printed control of the control of the control of the printed control of the control of the control of the printed control of the c
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Best Local Similarity
Matches 1182; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodirective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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food supplement; r
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)B; ABG19673.
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GGGGTTGGAAAGTCTTGCCTTCTTAGGTTTGCAGATGATACATATACAGAAAGCTAC
                                    ATGTCCAGCATGAATCCCGAATATGATTATTTATTCAAGTTACTTCTGATTGGCGACTCA
                                                           ATGTCCAGCATGAATCCCGAATATGATTATTTATTCAAGTTACTTCTGATTGGCGACTCA
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2000US-0649167
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medical imaging; diagnostic; genetic disorder;
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                                                    CTATGTAACAAAACAACTGAAGATATGTTTAATAAATATTGTACTTATTGGAAGT
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                                                                                                                                                                                                                                                                                      CAGCACAAGCAGTGTCTCACTTTCCATGCATAAAGTTTAGTGAGATGTTATATGTAAG
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28-MAR-2001;
29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutics compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating are immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Note: With the exception of SEQ ID No 1 and 2, the for this patent did not form part of the printed supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-2001; 2001WO-US24218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colon cancer polypeptides and polynucleotides, useful as diagnosing, preventing, and treating colon cancer, and as the progression of cancer -
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TCATTTTCAGAACTGTTTTAAACCTTTGTGTGCTGGTTTATAAAATAATGTGTGTAATCC
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2001US-279763P.
2001US-302051P.
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(GCA), by detecting the level of expression of gene(s) (Gs) identified DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of subject to a pathogen or sterile inflammatory disease using the
                                                                                                                                                                                                        Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-2001; 2001WO-US30821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiac reperfusion injury; renal reperfusion injury; ARD adult respiratory distress syndrome; inflammatory bowel d Crohn's disease; ulcerative colitits; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombos
                                                                                                                                                                                                                                                                                              Beazer-Barclay Y, Weissman SM,
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CC denote) in a tissue, an allergic response in a subject, exposure of a control of the tracking the control of expression in a sample of the tissue of gene(s) from GS, where control of expression in a sample of the tissue of gene(s) from GS, where control of expression of the gene is indicative of inflammation; where control of the tissue of gene(s) from GS, where control of the expression of the gene is indicative of inflammation; which a subject, exposure of a subject to a pathogen control of the tissue in a subject, exposure of a subject to a pathogen control of the tissue. All is useful for detecting GCA; AZ is useful for conducting GA; AZ is useful for the conducting GA; AZ is useful for the preference of a subject to a pathogen or sterile conformation and inflammation (especially chronic) in a tissue, an allergic conformation of the properties of a subject to a pathogen or sterile conformation injury, ARDS, adult respiratory distress syndrome, conditions to a pathogen or sterile conformation injury, also bacterial infection, viral infection, condities, periodontal disease; also bacterial infection, viral infection and M5 is conducted by the properties of the above conditions. The present conditions of the properties of the sequence data for this patent did not form part conditions the properties of the printed specification, but was obtained in electronic conditions the properties.

CC format directly from WIPO at the properties of the properties of the printed specification, but was obtained in electronic conditi
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613; Conserv
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                                                                        GATTCCCTTGGAATTCCGTTTTTGGAAACCAGTGCTAAGAATGCAACGAATGTAGAACAG
                                                                                                                                                                                                                            AACAAATGTGATCTGACCACAAAGAAAGTAGTAGACTACACAACAACAGCGAAGGAATTTGCT
                                                                                                                                                                                                                                                                                                                                      CAGTGGCTGCAGGAAATAGATCGTTATGCCAGTGAAAATGTCAACAAATTGTTGGTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTGGTGTGGATTTCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATCAAGCTTCAA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGTCTTGCCTTCTTAGGTTTTGCAGATGATACATATACAGAAAGCTACATCAGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGCTGCCAGCAAGCGCGGCGGCGGCGGCGCCAGCTGCAGTGACATGTCCAGC
TCTTTCATGACGATGGCAGCTGAGATTAAAAAGCGAATGGGTCCCGGAGCAACAGCTGGT
                                                                                                                                                                                           AACAAATGTGATCTGACCACAAAGAAAGTAGTAGACTACACAACAGCGAAGGAATTTGCT
                                                                                                                                                                                                                                                                                                     CAGTGGCTGCAGGAAATAGATCGTTATGCCAGTGAAAATGTCAACAAATTGTTGGTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                     GCCCATGGCATCATAGTTGTGTATGATGTGACAGATCAGGAGTCCTTCAATAATGTTAAA
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ilarity 84.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GAGTCCTTCAATAATGTTAAA 392
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Pred. No. 1.3e
0; Mismatches
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δõ 맑 δ 밁 Q 밁 δ 밁 Ş Б ρy 밁 Q 밁 õ Ъ Š 밁

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RESULT 5
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ID ABA430
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     The invention relates to a spatially-addressable set of single exon concluded acid probes for measuring gene expression in a sample derived from human breast and BP 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label count to each probe of the microarray. The probes are useful for encode proteins. They are useful for gene discovery, and for encode proteins. They are useful for gene discovery, and for econode proteins. They are useful for sensing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical compression analysis is useful for assessing the toxicity of chemical compression analysis. The microarray of this invention presents a far greater than expressed sequence tag microarrays. The method is suitable for the expressed sequence is a single exon nucleic acid probe of the invention. The sequence is a single exon nucleic acid probe of the invention. The sequence data for this patent did not form gart of the printed specification, but was obtained in electronic format directly considered the constant directly and the constant directly exon microarray in the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312; 26-MAY-2000; 2000US-00207456; 30-JUN-2000; 2000US-0608408; 03-AUG-2000; 2000US-0632366; 21-SEP-2000; 2000US-0234687; 27-SEP-2000; 2000US-0234539; 04-OCT-2000; 2000GB-0024263;
                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1791; 327pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                            New spatially-addressable set of single exon nucleic acid pruseful for measuring gene expression in sample derived from breast, comprises number of single exon nucleic acid probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human breast cell single exon nucleic acid probe #1791.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00662.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Chen
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RESULT 6
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                                                                      04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
            WPI; 2001-483447/52
                                                                                                                                                                                                                                                                        ABA53512 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                  30-JAN-2001;
                                                                                                                                                                   WO200157277-A2
                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                    Human foetal liver single exon nucleic acid probe #1817
                                             (MOLE-)
                             SG,
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                                             MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                CTGGTTTATAAAATAATGTGTGTAATCCTTGTTGCTTTCCTGATACC 968
                                                                                                                                                                                                                                                                                                                                                        TTATTCCCTTGACTCAAGACAGCTAACTTCATTTTCAGAACTGTTTTAAACCTTTTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                             CAACAGCTGGTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGT
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                                                                                                                                                                                                                                                                                                                                                TTATTCCCTTGACTCAAGACAGCTAACTTCATTTTCAGAACTGTTTTAAACCTTTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                   CAGATTCTTACCGTCTCCACAAAGGTCAGAGATTGTAAATGGTCAATACTGACTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGAACCCAAGTGAAAAAACAAAATTGCCTGAATTGTACTGTAGCTGCACTACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAATTTGCTGATTCCCTTGGAATTCCGTTTTTGGAAACCAGTGCTAAGAATGCAACGA
                            Hanzel DK,
                                                             2000US-0180312.

2000US-0207456.

2000US-0608408.

2000US-0632366.

2000US-0234687.

2000US-0236359.

2000GB-0024263.
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                                                                                                                                  2001WO-US00669
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
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Pred. No. 2.4e-55;
0; Mismatches 0;
                             Rank
                                                                                                                                                                                                    single
                                                                                                                                                                                                    exon nucleic
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RESULT 7
ABA23276/c
ID ABA23276 standard; DNA; 48
XX
AC ABA23276;
XX
DT 23-JAN-2002 (first entry)
XX
Probe #1742 for gene expre
XX
KW Human; gene expression; he
KW cardiovascular disease; hy
KW congenital heart disease;
XX
PN W0200157274-A2.
XX
PD 09-AUG-2001.
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Query Match
Best Local Similarity
Matches 467; Conserv
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 487 BP; 154 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
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 47
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                                                                                                                                                                                                           CAGGTGGAGGTTGCTAAAATTTGCCTCCATCCTTTTCTCACAGCAATGAATTTTGCAA
                                                                                                                                                                                                                                                                                                                                                                                     SEQ
CTGGTTTATAAAATAATGTGTGTAATCCTTGTTGCTTTCCTGATACC
                            CTGGTTTATAAAATAATGTGTGTAATCCTTGTTGCTTTCCTGATACC
                                                            TTATTCCCTTGACTCAAGACAGCTAACTTCATTTTCAGAACTGTTTTAAACCTTTGTGTG
                                                                                                                            CAGATTCTTACCGTCTCCACAAAGGTCAGAGATTGTAAATGGTCAATACTGACTTTTTTT
                                                                                                                                                                                                                                                        CAGGTGGAGGTTGCTGAAAATTTGCCTCCATCCTTTTCTCACAGCAATGAATTTGCAA
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                                                                                                                                                                                          Conservative
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          639pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 467; DB 22; pred. No. 2.4e-55; pred. No. 2.4e-55;
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487 BP.

(first entry)

Probe #1742 for gene expression analysis in human heart cell sample

Human; gene expression; heart; microa cardiovascular disease; hypertension; congenital heart disease; ss. microarray; vascular ension; cardiac arrhy system; probe;

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Query Match
Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and concentral heart disease, hypertension, cardiac arrhythmias and
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hearts
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Note: The sequence data for this patent did not specification, but was obtained in electronic for
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                  CTGGTTTATAAAATAATGTGTGTAATCCTTGTTGCTTTCCTGATACC
                                                                                                TTATTCCCTTGACTCAAGACAGCTAACTTCATTTTCAGAACTGTTTTTAAACCTTTGTGTG
                                                                                                                                                        CAGATTCTTACCGTCTCCACAAAGGTCAGAGATTGTAAATGGTCAATACTGACTTTTTTT
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                                                                                                                                                                                                                               CAACAGCTGGTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGT
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2000US-0207456.
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ilarity 100.0%;
Conservative
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   brain expressed exon; gene expression analysis; probe; rray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                           AGGAATTTGCTGATTCCCTTGGAATTCCGTTTTTGGAAACCAGTGCTAAGAATGCAACGA
                                                                                                                                                   ATGTAGAACAGTCTTTCATGACGATGGCCAGCTGAGATTAAAAAGCGAATGGGTCCCGGAG
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0; Mismatches
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1.4e-55;
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26-MAY-2000;
30-JUN-2000;
                                                                                     probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                       analyzing
                                                                                                                                                                                                                                                                                                                                                                                                microarray;
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                                    al Similarity
467; Conserv
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zing gene expression in human bone marrow -
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                                          Score 467; DB 22;
Pred. No. 2.4e-55;
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30-JUN-2000;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a
                                               Claim
                                                               analyzing
                                                                                            WPI;
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                                                                                                                                                                                                                                                             WO200157278-A2
                                                                                                                                                                                                                                                                                                Probe; human; microarray; gene expression; cervical epithelial cell;
cervical cancer; ss.
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zing gene expression in
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                                                                                                                                MOLECULAR DYNAMICS INC
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                                                               exon nucleic acid probes useful human cervical epithelial cells
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RESULT 11
AAI33136/c
ID AAI33136;

XX AAI33136;
XX 17-OCT-2001 (first entry XX DT 17-OCT-2001)
DE Probe #1822 used to measu XX genetic disorder; ss.

XX 9Probe; microarray; human; XX genetic disorder; ss.

XX 9C00157272-A2.

XX W0200157272-A2.

XX W0200157272-A2.

XX 9D-AUG-2001, 2001WO-US006 XX PPD 09-AUG-2001, 2000US-01803 PR 26-ABY-2000; 2000US-01803 PR 20-SEP-2000; 2000US-03034 PR 30-JUN-2000; 2000US-03034 PR 30-JUN-2000; 2000US-03034 PR 21-SEP-2000; 2000US-03236 PR 21-SEP-2000; 2000US-03236 PR 21-SEP-2000; 2000US-03236 PR 21-SEP-2000; 2000US-03236 PR 21-SEP-2000; 2000US-03236
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Matches 467
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences.
                                                                                                                                                          Probe #1822 used to measure gene expression in human placenta sample.
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2000US-0207456.
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0; Mismatches 0;
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RESULT 12
AAI01752/c
ID AAI01752;
XC AAI01752;
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XX Probe #1743 used to
XX Probe; human; breast
XX W Probe; human; breast
XX W Probess AX
XX Homo sapiens.
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The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                 Probe #1743 used to measure gene expression in human breast sample
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Probe; human; breast disease; breast cancer;
inflammatory disease; proliferative breast d
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nucleic acid expressed in the human lung; measuring gene expression in a contection of detectably labeled nucleic acids derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon exon microarrays having a probe with the exon, where a common pattern of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                     from human turning from human turning the novel set of probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a probes; the novel set of probes which hybridise at high stringency to a probes; the novel set of probes which hybridise at high stringency to a probes; the novel set of probes which hybridise at high string the approach in a probes; the novel set of probes which hybridise a high string gene expression in a probes; the novel set of probes which hybridise at high string the array with problem in the human lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
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2000US-236359P.
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RESULT 14
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CN Note: The sequence data for this patent did not form part CC of the printed specification, but was obtained in electronic CC format directly from WIPO at CC fire. wipo. int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 467
                             Human; 5' EST;
                                                                       06-OCT-2000
                     Human; 5' EST; expressed sequence tag; secreted protein;
gene therapy; chromosome mapping; ss.
                                               Human secreted protein 5'
                                                                                                            AAC06621 standard; cDNA; 335
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                                                                                                                                                             CTGGTTTATAAARAATGTGTGTAATCCTTGTTGCTTTCCTGATACC 968
                                                                                                                                                                                                                                                                             CAACAGCTGGTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGT
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                                                                                                                                                                                                            TTATTCCCTTGACTCAAGACAGCTAACTTCATTTTCAGAACTGTTTTAAACCTTTTGTGTG
                                                                                                                                                                                                                                                                                                                      CAGGTGGAGGTTGCTGCTAAAATTTGCCTCCATCCTTTTCTCACAGCAATGAATTTGCAA
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                                                  EST, SEQ ID NO: 10696.
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                                                                              ATCSWWGTTGCTTTCCTGATACCAGAYTGTTTCCC
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORR has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA ilbraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain pertream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 335 BP; 96 A; 70 C; 56 G; 109 T; 4 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid that is a 5'
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16-MAR-2000;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 2343-2344; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                Sequence 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2002
                                                                                                                                                                                                                                                                                                                                       patient;(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                 (e) selecting a composition for inhibiting prostate cancer in a patient;(f) assessing the prostate cell carcinogenic potential of a compound;(g) determining whether prostate cancer has metastasized in a patient;(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                          cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-2000
 758
                              226
                                                          869
                                                                                    286
                                                                                                                                       406
                                                                                                                                                                                                                                                         264;
                                                                                                                                                                                                                                                                     Similarity
                                                                                TGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCAGGTGGAGGTTGCTG
                                                                                                                                                                                                AAAACAAATTGCCTGAATTGTAC 781
                                        CTAAAATTTGCCTCCATCCTTTTCTCACAGCAATGAATTTGCAATCTGAACCCAAGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
                          CTAAAATTTGCCTCCATCCTTTTCTCACAGCAATGAATTTGCAATCTGAACCCAAGTGAA
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2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                                                                                                                                                                                                                                              BP;
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                                                                                                                                                                                                                                                    18.08; 1.00.08; 1.00.00;
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                                                                                                                                                                                                                                                       Score 264; DB
; Pred. No. 9.7
0; Mismatches
                                                                                                                                                                                                                                                                                                              92 G; 111
                                                                                                                                                                                                                                                                    DB 23;
9.7e-28;
                                                                                                                                                                                                                                                                                                              T; 0 other;
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Search completed: June 22, Job time : 356 secs 2003, 19:53:56

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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     a
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   743
732.4
727.6
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708.8
                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic search, using sw model
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Copyright (c) 1993 - 2003 Compugen Ltd.
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RESULT 1 AL539022 AL539022 AL539022 LTI_FL013_FBrn1 Homo sapiens CDNA clone CSODF030YG06 5 DEFINITION AL539022.1 LTI_FL013_FBrn1 Homo sapiens CDNA clone CSODF030YG06 5 Prime, mRNA sequence. ACCESSION AL539022.1 GI:12867866 EST. ORGANISM EST. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; AUTHORS HOMO sapiens FULL-length cDNA libraries and normalization COMMENT Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedax - France Email: seqref@genoscope.cns.fr, Heb : www.genoscope.cns.fr. JOURNAL COCATION (Joualifiers FEATURES SOURCE AUTHORS SOURCE FOLTOMALISM CONTACT: Contact: Genoscope BP 191 91006 EVRY cedax - France Email: seqref@genoscope.cns.fr, Heb : www.genoscope.cns.fr. JOURNAL COCATION (Joualifiers Colone="CSODF030YG06" Colone="C

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BASE COUNT
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Matches 849;
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AGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCAGGTGGAGGTTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGATCTGACCACAAAGAAAGTAGTAGACTACACAACAGCGAAGGAATTTGCTGATTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCAGGAAATAGATCGTTATGCCAGTGAAAATGTCAACAAATTGTTGGTAGGGAACAAAT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGATITCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATCAAGCTTCAAATA---- 371
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                                                                   AAAATTTGCCTCCATCCTTTTCTCACAGCAATGAATTTGCAATCTGAACCCAAGTGAAAA 759
                                                                                                                                                                                                                                                                                                                            TGACGATGGCAGCTGAGATTAAAAAGCGAATGGGTCCCGGAGCAACAGCTGGTGGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGAATTCCGTTTTTGGAAACCAGTGCTAAGAATGCAACGAATGTAGAACAGTCTTTCA 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGATCTGACCACAAAGAAAGTAGTAGACAACAACAGCGAAGGAATTTGCTGATTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCATCATAGTTGTGTATGATGTGACAGATCAGGAGTCCTTCAATAATGTTAAACAGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTTCTTCTTAGGTTTGCAGATGATACATATACAGAAAGCTACATCAGCACAATTGGTG
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                                                                                                                                                                                                                                                                                       TGACGATGGCAGCTGAGATTAAAAAGCGAATGGGTCCCGGAGCAACAGCTGGTGGTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end
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cDNA was primed with a NotI-oligo(dT) primer. Five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enriched, double-stranded cDNA was digested with Not cloned into the Not I and Eco RV sites of the VSPORT 6 vector. Library was constituted to the Not I and I and I are the Not I and I are the Not I
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No. 1.4e-78;
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E.E. Consortium/LLNL at: http://image.llnl.gov
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BQ014597.1 GI:19739498
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UI-H-ED1-axt-b-23-0-UI.sl NCI_CGAP_ED1 Homo
IMAGE:5833270 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (Dases 1 to ''')
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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1 (bases 1 to 777)
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                                                                                                   Similarity
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                     ATGCAACGAATGTAGAACAGTCTTTCATGACGATGGCAGCTGAGATTAAAAAAGCGAATGG
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                                                                                                                                                                                                                                    /lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI_CGAP_EDI is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_LIB-UI-H-EDI
TAG_TISTECTONATORSATORM
                                                                                                                                                                                   D
                                                                                                                                                                                 TAG_TISSUE-chondrosarcoma
TAG_SEQ~CGTCAAGGCT"
146 c 128 g 242
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_ED1"
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                                                                                                   52.1%;
98.6%;
                                                                            Score 732.4;
Pred. No. 2.8e
0; Mismatches
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JOURNAL COMMENT -
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                                                                                     Homo sapiens Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 811)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                       sequence.
AA746643
AA746643.1
EST.
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                                                                                                                                                                                                                                  AA746643 811 bp mrNA linear EST 22-JAN-1998 nx27c08.sl NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1257326 3' similar to gb:M28209 RAS-RELATED PROTEIN RAB-1A (HUMAN);, mrNA
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk,
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, F
cDNA Library Arrayed by: Greg Lennon, Ph.D.
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               Soares, Ph
                                        M.D.,
                                        Ph
                                        .<sub>D</sub>.,
                                        Michael
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DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.B. Consortium/LLNL at: NWW-bio.llnl.gov/bbrp/image/image.html Insert Length: 861 Std Error: 0.00 Seq primer: -40ml3 fwd. Er 'from Amersham High quality sequence stop: 471.
                                                                                                                                                                                                                                                                                                                                                     CTGGTTTATAAAATAATGTGTGTAATCCTTGCTTGCTTCCTGATACCAGACTGTTTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACAGCTGGTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGT
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TTTCCATGCATAAAGTTTAGTGAGATGTTAATATGTAAGATCTGATTTGCTAGTTCTTCCT
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                                                                                                                  CTGGTTTATAAAATAATGTGTGTAATCCTTGTTGCTTTCCTGATACCAGACTGTTTCCCG
                                                                                                                                                                                                   TGGTTGGTTAGAATATATTTTGTTTTGATGTTTATATTGGCATGTTTAGATGTCAGGTTT
                                                                                /Organism="Homo sapiens"
//db_xref="taxon:9666"
//dlone=Itb="NGGE:157326"
//clone=Itb="NGGE:157326"
//lab_host='DHO188"
//lab_
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95.8%;
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Pred. No. 9.8e
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1 (bases 1 to 817)
NIH-MGC http://mgc.nci.nih.gov.
National Institutes of Health,
Unpublished (1999)
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Plate: LLAM12030 row: p column:
High quality sequence stop: 669.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLA DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAAACCAGTGCTAAGAATGCAACGAATGTAGAACAGTCTTTCATGACGATGGCAGCTG
                                                                                                               AGAAAGTAGTAGACTACACAACAGCGAAGGAATTTGCTGATTCCCTTGGAATTCCGTTTT
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/clone="IMAGE:5404275"
/clone="imaGE:5404275"
/clone=lib="NIH_MCC_90"
/clone_lib="NIH_MCC_90"
/tissue_type="adenocarcinoma, cell line"
/lab_host="PHHIOB (phage-resistant)"
/note="Organ: Liver; Vector: pcMv-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
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Note: this is a NIH_MGC Library."
155 c 169 g 256 t .
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95.3%;
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Pred. No. 2.7e-76;
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BQ276678
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1 (bases 1 to 910)
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High quality sequence
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FEATURES
                            cDNA Library Preparation: Michael Brownstein Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E.. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2055 row: i column: 22
                                                                                                                                                                   Tissue Procurement: NCI
                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
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Primates;
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TTACACTATCTGATTAATAGTTTCTTCATACTCTGCATATAATTTTGTGGCTGCAGAATAT
                                                                                   GCCATTTTGTATCAAACAGCACAAGCAGTGTCTGTCACTTTCCATGCATAAAGTTTAGTG 1123
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Seq primer: M13 FORWARD
POLYA*Yes.
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1244 TGTAATTTGTTGCACACTATGTAACAAAACAACTGAAGATA-TGTTTAATAATATTGTA 1302
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Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 761)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept..of
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                                                                                                                                                                                                                                                                                                     /note-*Organ: Left Pelvis; Vector: py7773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_Ch2 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)8 tail. The sequence tag for this library is
                                                                                                                                                             TAG_LLB=UI-H-EZ1
TAG_TISSUE-grade-2-chondrosarcoma
TAG_SE0-ATCTNATATG*,
143 c 125 g 235 t
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/db_xref="taxon:9606"
/clone="U1+"E21-bbk-1-10-0-UI"
/clone=1lb="NCI_CGAP_Ch2"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (Life Technologies)"
          Score 708.4; DB 1
Pred. No. 1.8e-74;
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AL530265 LTI_NFL001_NBC4 F Prime, mRNA sequence.
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
Location/Qualifiers
                                                      Eukaryota; Metazoa; Chordata; Craniata; Verte Mammalia; Eutheria; Primates; Catarrhini; Hon 1 (bases 1 to 945)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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                    ACAGCTGGTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCA
                                                     GTAGAACAGTCTTTCATGACGATGGCAGCTGAGATTAAAAAGCGAATGGGT-CCGGAGCA
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         ACAGCTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCA
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODDD09YH19"
/clone_lib="LTI_NFL001_NBC4"
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/lab_host="DH10B"
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Oy Oy Oy	Query Match Best Local Matches 89	BASE COUNT	FEATURES source		REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 8 BM452262	D	оу Оу оу
1 AAGCGATAGCTGAGT-GCGGCGGCTGCTGATTGTGTTCTAGGGGAACAGAGTAGGGGAAGA 59	Query Match 50.1%; Score 704.4; DB 13; Length 1105; Best Local Similarity 86.0%; Pred. No. 4.1e-74; Matches 899; Conservative 0; Mismatches 43; Indels 103; Gaps 7;	/Lissue_type="melanotic melanoma" /lab_host="DHINB (phage-resistant)" /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Sverage insert size 2 kb. Library constructed by Life Pechnologies." 320 a 216 c 279 g 282 t 8 others	Plate: LI High qual	remail: ggapbs-remail.nin.gov Tissue Procurement: ATCC/DCTD/DTP CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	Eukaryo Mammali 1 (bas NIH-MGC Nationa Unpubli Contact	N AGENCOURT_6386191 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5526 5', mRNA sequence. 1 BM452262 BM452262 BM452262.1 GI:18501302 EST. human. h Homo sapiens	M452262		684 -GGTGGAGGTTGCTGCTAAAATTTGCCTCCATCCTTTTCTCACAGCAATGAATTTGCCAAT 742
RESULT 9 EQ448090/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Db	Qy Qy Db	Qy Db Db		ов Оу Оу	Db Qy Ov	Qy Dy	ор Оу	о Оу Оу
/C BQ448090 725 bp mRNA linear EST 29-MAY-2002 ON UI-H-EU1-bai-k-14-0-UI.sl NCI_CGAP_Ctl Homo sapiens cDNA clone UI-H-EU1-bai-k-14-0-UI 3', mRNA sequence. N BQ448090 BQ448090.1 GI:21251202 EST. human. human sapiens	920 TGCTGGTTTATAAAATAATGTGTGT 944 1	803 AGATTCTTACCGTCTCCACAAAGGTCAGAGATTGTAAATGGTCAATACTGACTTTTT 860	684 - GGTGGAGGTTGCTGCTAAAATTTGCCTCCATCTTTTCTCACAGGAATGAAT	564 GTAGAACAGTCTTTCATGACGATGCAGCTGACATTAAAAGCGAATGCGTCCCGGAGCA 623	TIGGTAGGAACAAATGTGATCTGACCACAAAGAACCAGTGCTAAGAATGCAACGAATGTATTTGCTGATTCCCTTGGAATTCCGTTTTTGGAAACCAGTGCTAAGAATGCAACGAACG	422 TACAGAGGAGCCCATGGCATCATAGTTGTGTATGATGTGACAGATCAGGAGTCCTTCAAT 481 384 AATGTTAAACAGTGGCTGCAGGAAATAGATCGTTATGCCAGTGAAAATGTCAACAAATTG 443	372	GGGGTTGGAAAGTCTTGCCTTCTTTAGGTTTGCAGATÄGÄTÄČÄTÄTÄCÄĞÄAÄĞCTÄC ATCAGCACAATTGGTGGGATTTCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATC	122 AGTCAGGGCGGCGGCGGGAGCAAGCAAGGGCGGCGGGGGGGG

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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mmalia; Eutheria;
(bases 1 to 725)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_TISSUE-osteoarthritic cartilage
TAG_SEQ-TGATCACGCT"
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/clone="UI-H-EU1-bai-k-14-0-UI"
/clone_lib="NCI_CGAP_Ct1"
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/db_xref="taxon:9606"
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1. (bases 1 to 796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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National Institutes of Health, Mammalian
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/db_xref="taxon:9606"
/clone="IMAGE:5244094"
/clone=1ib="NIH_MGC_121"
/lab_host="DH10B"
             directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber
                                                                                               /note-"Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and male age 26 weeks.
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was constructed by 
Genetics tracking
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  MM971301 760 bp mRNA
UI-CF-EC1-abl-a-17-0-UI.S2 UI-CF-EC1 Homo
UI-CF-EC1-abl-a-17-0-UI 3', mRNA sequence.
BM971301 GI:19588888
EST.
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Pred. No. 9.8e-74;
0; Mismatches 30;
                                                                                 RNA linear
Homo sapiens
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ORGANISM
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Best Local Similarity 99.1%;
Matches 738; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                             648 AATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCAGGTGGAGGTTGCTGCTAAAATTTG
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University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
7cl: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of
DNA Sequencing by: Dr. M. Bento Soares, University of
DNA Sequencing by: Dr. M. Bento Soares, University of
DNA Sequencing by: Dr. M. Bento Soares, University of
DNA Sequencing by: Dr. M. Bento Soares, University of
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 760)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)
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Homo sapiens
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                                                                                                                                                                                                  GCAGCTGAGATTAAAAAGCGAAT-GGTCCCGGAGCAACAGCT-GTGTGNCTGAGAAGTCC
                                                                                                                   ATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCAGGTGGAGG-TGCTGCTAAAA-TTG
TGCCTGAATTGTACTGTATGTAGCTGCACTACAACAGATTCTTACCGTCTCCACAAAGGT
                                        255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Lung"
//dev_stage="Adult and Fetal"
//dev_stage="Adult and Fetal"
//dev_stage="Adult and Fetal"
//lab_host="philds (Life Technologies) (TI phage resistant)"
//lab_host="philds (Life Technologies) (TI phage resistant)"
//lab_host="philds (Life Technologies) (TI phage resistant) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
//lab_host="philds (Life Technologies) (Life Technologi
                                                                                                                                                                                                                                                                                                                                                                                      TAG_SEQ=AAGTGCTTAC"
142 c 125 g
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TAG_TISSUE-Normal Lung
and 380-383
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/db_xref="taxon:9606"
/clone="UI-CF-EC1-abl-a-17-0-UI"
/clone_11b="UI-CF-EC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Pred. No. 1.26
0; Mismatches
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1 (bases 1 to 976)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                      5', mRNA sequence.
BM919860
BM919860.1 GI:193
                                                                                 High
                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                  Contact: Robert Strausberg,
                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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LLAM12779 row: f column:
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                          AAAATTTGCCTCCATCCTTTTCTCACAGCAATGAATTTTGCAATCTGAAACCCAAGTGAAAA
                                                                               AGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCAGGTGGAGGTTGCTGCT
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              AAAATTTGCCTCCATCCTTTTCTCACAGCAATGAATTTGCAATCTGAACCCCCCAGTGAAA
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----GAGTCCTTCAATAATGTTAAACAGTGGC

399 432 371 372 371 312 315 252 255

459

672 639

852

792 699 732 579

612 519 552 /note**Organ: pooled pancreas and spleen; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library.*

a 196 c 246 g 248 t 1 others /lab_host="DH10B"

18;

Indels Length

100;

Gaps

195

192

617 CGGAGCAACAGCTGGTGGTGCTGAAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAA	FEATURES SOURCE 1837 ACGARTGTRAGAACAGGGTGGGAGGTGGAGATTAAAAAGCGAATGGGTCG 60 Location / Qualifiers 1837 Acgartanacan 1606* Adb_xref="Homo sapiens" Adb_xref="Homo sapiens" Account Index Account Account Account Index Account Account Index Account Account Index Account Account Index Index Account I	SULT 13 B1086445 B108644	Db 853 AACAAATTGCCTGAATTGTACTGGATGTAGCTGCACTACAAGAATTCTTACCGTCTC 912 Oy 819 CACAAAGGTCAGAGATTGTAAATGGTCAATACTGACTTTTTTTTTAT 865
soare rocur brary brary puency istry (www ner: N Loca /db_ /clc	BM706159 BM706159 BM706159 BM706159 BM706159 DEFINITION UI-E-DM0-agg-f-10-0-UI-5', mRNA sequence. ACCESSION BM706159 WERSTON BM706159.1 GI:19019417 KEYMORDS SOURCE ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 689) AUTHORS TITLE BONAICAM.F., Lennon,G. and Soares,M.B. VOURNAL MEDLINE JOURNAL Genome Res. 6 (9), 791-806 (1996) COMMENT CONTACT: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA	361 GTGTGGTTATAAATTGTAAATATGTAATTGTAATTATAAAAAA	Qy 857 TTTTTTATTCCCTTGACTCAAGACAGCTAACTTCATTTCAGAACTGTTTTAAACCTTT 916

BASE COUNT ORIGIN

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Query Match
Best Local Similarity
Matches 689; Conserv
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                       GGTTGGTTAGAATATATTTGTTTTGATGTTTATATTGGCATGTTTAGATGTCAGGTTTA 1042
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                                                             GTAGAGTTATAAATGGAAAGATTACACTA 1191
                                                                                                                    TTCCATGCATAAAGTTTAGTGAGATGTTATATGTAAGATCTGATTTGCTAGTTCTTCCTT 1162
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/dev_stage="adult"
/dev_stage="adult"
/dev_stage="millow (Life Technologies) (TI phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-DWO is a cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an ollyo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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%; Pred. No. 3.6e-72;
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High quality sequence stop: 727.
Location/Qualifiers
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1 (bases 1 to 737)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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602856302F1 NIH_MGC_10 Homo sapiens
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                 AACCTTTGTGTGCTGGTTTATAAAATAATGTGTGTAATCCTTGTTGCTTTCCTGATACCA
                                                       CTGACTTTTTTTTTATTCCCTTGACTCAAGACAGCTAACTTCATTTTCAGAACTGTTTTA
                                                                                                                                  GCTGCACTACAACAGATTCTTACCGTCTCCACAAAGGTCAGAGATTGTAAATGGTCAATA
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/cell_line="MGC36"
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/db_xref="taxon:9606"
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastseQ for Windows Version 2.0

CURRENT APPLICATION NUMBER: US/08/916,901

FILING DATE: Filed Herewith

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE: APPLICATION DATA:

APPLICATION NUMBER: 35,749

REGISTRATION NUMBER: 35,749

REGISTRATION NUMBER: BF-0367 US

REGISTRATION NUMBER: BF-0367 US

REGISTRATION NUMBER: BF-0367 US

TELEPHONE: 415-845-4166

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LENGTH: 2514506

US-08-916-901-4
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US-08-916-901-4
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Patent No. 5
GENERAL INI
Query Match 13.9%;
Best Local Similarity 63.5%;
Matches 389; Conservative
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STATE: CA
COUNTRY: USA
COUNTRY: 94304
TD: 943D#
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ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
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APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
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US-09-463-238-3

US-08-280-443-1

US-08-457-459-1

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US-08-55-678-1

PCT-US95-02275-1

US-09-376-259-1

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Query Match

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Pred. No. is the number of results predicted by chance to I score greater than or equal to the score of the result beliand is derived by analysis of the total score distribution

SUMMARIES

195 195 102.2 102.2 102.2 100.4 100.

US-08-916-901-4
US-09-156-729-28
US-09-506-729-29
US-09-506-729-29
US-09-506-729-29
US-09-506-729-39
US-08-628-417-5
US-08-628-417-5
US-09-247-3738-33
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US-08-652-1968-12
US-08-61-1968-12
US-08-194-1968-12
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US-09-347-803-11
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US-09-370-838-151
US-09-79-906-1
US-09-917-180-1

Sequence

1, A 9, A 1, A 27, A 95, A

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Database

Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
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Title: Perfect score:

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Scoring table:

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RESULT 2
US-09-154-602-4
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Patent No. 6300472
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    APPLICANT: Corley,
APPLICANT: Shah, Pu
TITLE OF INVENTION:
                                                                                                                           COMPUTER READABLE FORM
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    APPLICATION DATA:
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Shah, Purvi
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IBM Compatible
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US-09-506-729-59

; Sequence 59, Application US/09506729

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J.

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0

TELECOMMUNICATION: INFORMATION:

TELEPHONE: 415-855-055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/9: FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: LIVE 2514506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 CCAGCATGAATCCCGAATATGATTATTTATTCAAGTTACTTCTGATTGGCGACTCAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 389;
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                                                                                                              GAGGTTGCTGCTA
                                                                                                                                                                                                                                          AACAGTCTTTCATGACGATGGCAGCTGAGATTAAAAAGCGAATGGGTCCCGGAGCAACAG
                                                                                                                                                                                                                                                                                                       TTGCTGATTCCCTTGGAATTCCGTTTTTTGGAAACCAGTGCTAAGAATGCAACGAATGTAG
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                                                                                            GTGGCTGTTGCTA
                                                                                                                                                          CTGGGGG----CGAGCGGCCCAATCTCAAGATCGACAGCACCCCTGTAAAAGCCGGCTGGCG
                                                                                                                                                                                     CTGGTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCAGGTG
                                                                                                                                                                                                                       AGCAGGCGTTCATGACCATGGCTGCTGAAATCAAAAAGCGGATGGGGCCTGGAGCAGCCT
                                                                                                                                                                                                                                                                                    TTGCAGACTCTCTGGGCATCCCCTTCTTGGAGACGAGCGCCAAGAATGCCACCAATGTCG
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Pred. No. 1e-30;
0; Mismatches 1
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657 687 600 627 540 567 480 507 420 447 360 387 300 371 240 363 180

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CURRENT APPLICATION NUMBER: US/09/506,729
CURRENT APPLICATION NUMBER: US/09/506,729
CURRENT FILING DATE: 2000-02-18
EARLIER APPLICATION NUMBER: ECT/US98/17284
EARLIER FILING DATE: 1998-08-21
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 59
LENGTH: 171
TYPE: DNA
ORGANISM: HOMO Sapiens
US-09-506-729-59
                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/506,729
CURRENT FILING DATE: 2000-02-18
CARLIER APPLICATION NUMBER: PCT/US98/17284
EARLIER FILING DATE: 1998-08-21
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 28
LENGTH: 166
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; ORGANISM: Homo sapiens
US-09-506-729-28
                                                                  Query Match
Best Local S
Matches 166
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APPLICANT: Welssman, Sherman M.
TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE
TITLE OF INVENTION: GRANULOCYTIC CELLS
FILE REFERENCE: 44921-5016-US
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APPLICANT: Weissman, Sherman M.
TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN
TITLE OF INVENTION: GRANULOCYTIC CELLS
FILE REFERENCE: 44921-5016-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yerramilli, Subrahmanyam V.
APPLICANT: Prashar, Yatindra
APPLICANT: Newberger, Peter
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                                                                     al Similarity
166; Conserv
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65352
                                                             11.8%; Score 166; DB 4; Length 166; llarity 100.0%; Pred. No. 4.3e-25; Conservative 0; Mismatches 0; Indels
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WESULT 6
US-08-628-417-5
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MOLECULE TYPE:
DESCRIPTION:
US-09-363-708-3
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US-09-363-708-3
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Best Local Similarity 88.8%;
Matches 111; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (312) 474-0448: INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2246 base pairs
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NAME: Clough, David W.
REGISTRATION UNDER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34451
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/363,708
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233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States of America
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/desc = "mouse PAL cDNA"
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US-08-628-417-6
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US-08-628-417-5
                                                                                                                                                                                      Sequence 6, Application US/08628417 Patent No. 5627054
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MOLECULE TYPE: Oli
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TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                       APPLICANT: GILLESPI
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 398-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL ADDRESSEE: DEFENSE COMMAND STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC) CITY: ABERDEEN PROVING GROUND
                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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COUNTRY:
                STATE:
                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                           SSEE: DEFENSE COMMAND
T: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
ABERDEEN PROVING GROUND
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                                                                                                                     COMPETITOR PRIMER ASYMMETRIC POLYMERASE CHAIN REACTION
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Pred. No. 2.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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; SEQ ID NO 1; LENGTH: 1872; TYPE: DNA; ORGANISM: Human US-09-801-052-1
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US-09-801-052-1
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                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: CLOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 116; Conserv
                                                                                Query Match
                                                      Matches
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09801052 Patent No. 6368842
                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/801,052
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1327
1712 CCCACTTTCCAGGGCAAAAAGGGCCCAGGGTTATAATAAGTAAATAACTTGTCTGTAAAA 1771
                         1387 AAAAAAAAAAAAAAAAA 1405
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                                                                    Similarity
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                                                      Conservative
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                                                                                                                                                                                                                                                                                            Ellen
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83.5%;
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                                                   Score 102; DB 4;
Pred. No. 5.7e-12;
0; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 102.2;
Pred. No. 3e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                Length 1872;
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                                                      Indels
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US-08-157-101A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOTBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: MICrosoft Office 97
SEQ ID NO 33
LENGTH: 1117
TEUE: NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.2%;
Best Local Similarity 73.3%;
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (1101)
OTHER INFORMATION: M=A OR C
NAME/KEY: unsure
LOCATION: (1104)
OTHER INFORMATION: M=A OR C
                                                                                                                                                                                         equence 4, Applicati
atent No. 5808032
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MCGONIGLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (1116)
                                    ITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION ITLE OF INVENTION: PLASMIDS THEREFOR THESE OF SEQUENCES: 9

TREES FOR THE OF T
                  DDRESSEE:
                                                                                                                                                                                                                                                                                                                                              1230 TGGCTGCAGAATATTGTAATTTGTTTGCACACTATGTAACAAAACAACTGAAGATATGTTT 1289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1376 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1405
                                ESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                914 TTGATGTCAATTATCCTACTCTTATGTAGCTTAACTAATAATATATTTATATTGATGGC 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33, Application US/09247373B
5. 6168954
                                                                                                                                                                                                                                                                                                               Application US/08157101A
1100 NEW YORK AVENUE, N.W.
                                                                                                                    TSURUOKA, NO
ARIMA, KENJI
                                                                                                                                                    KURIHARA, TATSUYA
MATSUKURA, SHIGEKAZU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRIAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 47; Indels
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Pred. No. 8.6e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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US-09-071-224-3
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TELEX: 6714627 CUCH
TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1066 base pairs
TYPE: nucleic acid
TYPE: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Sim.
Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3
      COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for W:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymor-
STRFFF
                                                                                                                COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lok, S1
APPLICANT: Presnell,
                                                                                                                                                                                 STREET: 1201 Ea
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                       REPLICANT: Foster, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTOR5
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.1%; Score 100.4; DB 1; Length 1066; Similarity 90.7%; Pred. No. 1e-11; O7; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09071224 6271343
                                                                                                                                                                                                                     E: Zymogenetics
1201 Eastlake Ave East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                          Gilbert,
                                                                                                                                                                                                                                                                                                                                                              Presnell, Scott R.
Jelmberg, Anna C.
Gilbert, Teresa
                                                                                               IBM Compatible
                                                DOS
for Windows Version 2.
                                us/09/071,224
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ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

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US-08-964-127-5
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08964127 Patent No. 6277565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.1%;
Best Local Similarity 87.3%;
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1813 base pair
                                                                                                                                                                                               ZIP: 02110-2804

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
NAME: Crews, Ph.D., L. Lee
REGISTRATION NUMBER: P-43,567
REFERENCE/DOCKET NUMBER: 0733
TELECOMMUNICATION INFORMATION:
                                                                                           APPLICATION NUMBER: US/08/964,127
FILING DATE: 06-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                 ATTORNEY/AGENT INFORMATION: NAME: Crews, Ph.D., L. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Coding Sequence LOCATION: 88...1362 OTHER INFORMATION:
                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                     225 Franklin Street
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Pred. No. 1.2e-11;
0; Mismatches 16;
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; LOCATION:
US-08-964-127-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Approx. No. 6313271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 112; Conserv
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APPLICANT: Grande
                                                      TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                NAME: Crews, Ph.D., L. Lee REGISTATION NUMBER: P-43,5 REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION: 617/542-5070
                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTEED for Windows Version 2.0b
CURRENT APPLICATION DATA:
                        SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pair
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Crews, Ph.D., L. L
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                      TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                               STREET: 225
CITY: Boston
STRANDEDNESS:
                                                                                                                                                                                        APPLICATION NUMBER: 08/9 FILING DATE: 06-NOV-1997
                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02110-2804
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TELEFAX: 617/542-8906
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FENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
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84.88;
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Pred. No. 1.3e-11;
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TELEPAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-545-196B-10
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US-09-496-692-5
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Best Local Similarity 84.8%;
Matches 112; Conservative
                                                       Matches 110;
                                                                       Query Match
Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22040-0747
COMPUTER READABLE FORM:
COMPUTER TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/545
FILING DATE: 19-CT-1995
CLASSIETCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
UMAER OF SEQUENCES: 65
STREESPONDENCE ADDRESS:
ADDRESSEE BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
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Similarity 86.6%;
10; Conservative
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Pred. No. 1.3e-11;
                                                      Score 99.8; DB 3;
Pred. No. 1.5e-11;
0; Mismatches 17;
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Search completed: June 22, 2003, 21:27:47 Job time: 97 secs
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US-08-545-196B-12
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Best Local Similarity 86.6%;
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MELKI, JULLIA
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE:
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: FARACI, C. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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PE: cDNA
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Pred. No. 1.5e-11;
0; Mismatches 17;
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Maximum DB seq length: 2000000000
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             Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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12 US-10-033-528-37
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13 US-09-96-632-4644
14 US-10-040-862-4644
15 US-09-918-995-4909
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17 US-09-918-995-2704
18 US-09-918-995-2704
18 US-09-918-995-2704
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Sequence 1742, Ap
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GGGTTGGAAAGTCTTGCCTTCTTTCTTAGGTTTGCAGATGATACATATACAGAAAGCTACA
                                                                 TGTCCAGCATGAATCCCGAATATGATTATTCAAGTTACTTCTGATTGGCGACTCAG
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	CTGCGG CTGCGG	GAACAG GAACAG	GTGCGG	100.0%; 100.0%; ive	US/0982 2A1 2A1 cennady e collared H UCLEIC A ROTEINS, 96 2001-03- 39 Windows			
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US-09-820-003A-3
US-09-820-003A-3
Sequence 3, Application US/09820003A
Patent No. US20020142382A1
GENERAL IMFORMATION:
APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001196-
CURRENT APPLICATION NUMBER: US/09/820,003A
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
TEMBERTH: A6050
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TYPE: DNA

ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(46050)
COTHER INFORMATION: n = A
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                                  TGGTTGGTTAGAATATATTTGTTTTGATGTTTATATTGGCATGTTTAGATGTCAGGTTT
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Sequence 37, Application US/09820003A
Patent No. US20020142382Al
GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISCLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THE
FITTLE OF INVENTION: PROTEINS, AND USES THEREOF
FILL REFERENCE: CLO01196
CURRENT APPLICATION UNBER: US/09/820,003A
CURRENT APPLICATION NUMBER: US/09/820,003A
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 39
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 601
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                                                    GCTAGTTCTTCCTTGTAGAGTTATAAATGGAAAGATTACACTATCTGATTAATAGTTTCT
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Pred. No. 4.2e-92;
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US-09-920-300A-374/c
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APPLICANT: Meagh
APPLICANT: Xu, J
APPLICANT: Secri
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TITLE OF INVENTION: AND DIGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 374
LENGTH: 506
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GENERAL INFORMATION:
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Meagher, Madeleine
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Pred. No. 8.7e-78;
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Query Match Best Local Matches

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US-09-864-761-1742/c
; Sequence 1742, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
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US-10-033-528-374/c
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APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 374
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             APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
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    TITLE
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ORGANISM: Homo sapiens
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    OF INVENTION:
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Pred. No. 8.7e-78;
Pred. No. 8.7e-78;
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ORGANISM: Homo :
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APPLICATION NUMBER: US (
FILING DATE: 2000-06-30
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APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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SEQ ID NOS: 49117
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ED IN HEART, SIGNAL = 2.3
ED IN BONE MARROW, SIGNAL = 2.3
ED IN LUNG, SIGNAL = 2.6
ED IN BRAIN, SIGNAL = 2.6
ED IN ADULT LIVER, SIGNAL = 1.9
ED IN BT474, SIGNAL = 6.4
ED IN PLACENTA, SIGNAL = 3.3
ED IN PLACENTA, SIGNAL = 3.3
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CAACAGCTGGTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGT

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APPLICANT: Algate, Paul A.
APPLICANTON COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTIONS: COMPOSITION AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION NUMBER: 60/186, 126
PRIOR APPLICATION NUMBER: 60/190, 479
PRIOR APPLICATION NUMBER: 60/200, 545
PRIOR APPLICATION NUMBER: 60/200, 303
PRIOR APPLICATION NUMBER: 60/200, 779
PRIOR APPLICATION NUMBER: 60/200, 799
PRIOR APPLICATION NUMBER: 60/200, 999
PRIOR APPLICATION NUMBER: 60/206, 201
PRIOR APPLICATION NUMBER: 60/206, 201
PRIOR APPLICATION NUMBER: 60/206, 201
PRIOR APPLICATION NUMBER: 60/218, 950
PRIOR APPLICATION NUMBER: 60/221, 903
PRIOR APPLICATION NUMBER: 60/222, 903
PRIOR APPLICATION NUMBER: 60/223, 316
PRIOR APPLICATION NUMBER: 60/223, 3178
PR
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PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4644
LENGTH: 367
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Publication No. US20020198362A1
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        0; Indels
                                                                        Length 367;
        0;
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        0;
                    FILTURE OF INVENTION: REGISTORY
FILE REFERENCE: 014058-01352005
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT PELLING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR PELLING DATE: 2000-03-17
PRIOR PELLING DATE: 2000-04-27
PRIOR PELLING DATE: 2000-04-27
PRIOR PELLING DATE: 2000-04-27
PRIOR PELLING DATE: 2000-04-28
PRIOR PELLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PELLING DATE: 2000-04-28
PRIOR PELLING DATE: 2000-04-28
PRIOR PELLING DATE: 2000-04-28
PRIOR PELLING DATE: 2000-04-28
PRIOR PELLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/20,099
PRIOR PELLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR PELLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR PRILING DATE: 2000-05-03
PRIOR PELLING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR PRIOR PARE: 2000-08-07
PRIOR PELLING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-10-040-862-4644
(Sequence 4644, Application US/10040862
Publication No. US20030078396A1
(GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Compositions and Methods for the Detection, Diagnosis and TITLE OF INVENTION: Lematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
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SEQ ID N
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    for Windows Version
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Query Match Best Local Similarity Matches 367; Conserv

TYPE: DNA ORGANISM: Homo sapiens -09-796-692-4644

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> 107 862 167 802 227 742 287 682 347

RESULT 7 US-09-796-692-4644

GENERAL INFORMATION:

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Sequence 4909, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4909
LENGTH: 436
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                                                                                                                                                                  ; NAME/KEY: misc_feature
; LOCATION: (1)...(436)
; OTHER INFORMATION: n =
US-09-918-995-4909
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US-09-918-995-4909
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                                                                                                          Matches
                                                                                                                                      Query Match
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                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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              TTTGCTCTCCCGGAACAGCCTATCTCATTCCTTTCTTTCGATTACCCGTGGCGCGGAGAG
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Conservative
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5427
LENGTH: 353
TYPE: DNA
ORGANISM: Bos taurus
108-09-960-352-5427
US-09-960-352-5427
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                      1186 ACACTATCTGATTAATAGTTTCTTCATACTCTGCATATAATTTGTGGCTGCAGAATATTG 1245
                                                                                                                                                 1126 ATGTTATATGTAAGATCTGATTTGCTAGTTCTTCCTTGTAGAGTTATAAATGGAAAGATT 1185
                                                                                                                                                                                                             1066 CATTITGTATCAAACAGCACAAGCAGTGTCTGTCACTTTCCATGCATAAAGTTTAGTGAG
                                                                                                                                                                                                                                                                      1006 TTGATGTTTATATTGGCATGTTTAGATGTCAGGTTTAGTCTTCTGAAGATGAAGTTCAGC
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                                                                                                                                                                                                                                                        60 TTGATGTTTATATTGGCATGTTTAGATGTCAGGTTTAGTCTTCTGAAGATGAAGTTCAGC
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                             CATTTTGTATCAAACAGCACCAGCGTGTCTGTCACTTTCCATGCATAAAGTTTAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCCAGCATGAATCCCGAATATGATTATTTATTCAAGTTACTTCTGATTGGCGACTCAGG
            ATGTTATATGTAAGATCTGATTTGCTAGTTCTTCCTTGTAGAGTTATAAACGGAAAGATT
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                                                                        ACACTATCTGATTAATAGTTTCTTCATACTCTGCATATAATTTGTGGCTGCAGAATATTG
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 6e-49;
0; Mismatches
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Indels

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RESULT 12
US-09-918-995-2704
Sequence 2704, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PETLICATION NUMBER: US/09/918,995
CURRENT PETLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 483
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: ORGANISM: Bos taurus
: OTHER INFORMATION: Clone ID: 38-LIB34-021-Q1-E1-B6
US-09-960-352-8911
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Patent No. US20020137139A1
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Wathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
APPLICANT: MINISTER AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 8911
LENGTH: 427
TYPE: AND
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Best Local 9
       FEATURE:
NAME/KEY: misc_feature
                                               ORGANISM: Homo sapiens
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Local Similarity 94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 TGGATTTCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATCAAGCTTCAAATA 371
301 TGGATTTCAAAATAAGAACTATAGAGTTAGATGGGAAAACAATCAAACTTCAAGATTA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GCCTTCTTCTTAGGTTTGCAGATGATACATATACAGAAAGCTACATCAGCACAATTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ACAGCCTATCTCATTCCTCTCCTTCGACTACCCGTGGCGCGAGAGTCAGGGCGGCGGCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 314.8; DB 10; Length 427; Pred. No. 4.4e-45; 0; Mismatches 17; Indels 2;
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US-09-918-995-34631
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US-09-918-995-34631
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HYSOG, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILLING DATE: 1999-01-20
NUMBER OF SED ID NOS: 38054
SOFTWARE: FBSISEQ for Windows Version 3.0
SED ID NO 34631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34631, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (1)...(459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
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                       105 ACCCGTGGCGCGGAGAGTCAGGGCGGCGGCGGCTGCGGCAGCAAGGGGCGGCGGTGGCGGCGGC 164
tch 20.0%; score 280.4; DB 9 al Similarity 91.4%; Pred. No. 3.5e-39; 296; Conservative 0; Mismatches 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 TATACAGAAAGCTACATCAGCACAATTGGTGTGGATTTCAAAATAAGAACTATAGAGTTA 344
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                                                                                                                                                                                                                       80 CGAGGCGCGGAGAGTTAAGGCGGTTGCTGCGGCATCAAGGGCGGCGGCGGCGGCGGCGGC
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                                                        RESULT 15
US-10-079-623-231
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: LOCATION: 2, 88, 216, 219, 247, 283
: OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-4584
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US-09-294-093B-4584
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SEQ ID NO 4584
LENGTH: 290
            Sequence 231, Application US/10079623 Patent No. US20020169302A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL PILE REFERENCE: PI-0009 US
CURRENT FILLING NATE: 1999-04-16
CURRENT FILLING DATE: 1999-04-16
FRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILLING DATE: APILI 21, 1998
NUMBER OF SEQ ID NOS: 6207
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
OTHER_INFORMATION: Incyte ID No. US20010051335A1 700354602H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                 61 AAAAAGCGAATGGGTCCCGGAGCAACANCTGGTGGTGGCTGAGAAGTCCAATGTTAAAAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAGAAAGCTACATCAGCACAATTGGTGTGGATTTCAAAATAAGAACTATAGAGTTAGAC
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                                                                                                                                                                             TTCTCACAGCAATGAATTTGCAATCTGAACCCAAGNGANAAAACAAAATTGCCTGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERL Program
Ilkka
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 261; DB 10;
Pred. No. 6.3e-36;
0; Mismatches 6;
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-623-231
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Best Local Similarity
Matches 281; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: mammary gland and methods for the
TITLE REPERENCE: 11000.1044c3
CURRENT APPLICATION NUMBER: US/10/079,623
CURRENT FILING DATE: 2002-02-19
CURRENT FILING DATE: 2002-02-19
   241
                                  254
                                                                       181
                                                                                                        194
                                                                                                                                             121
                                                                                                                                                          134 CTGCGGCAGCAAGGGCGGCGGTGGCGGCGGCGGCAGCTGCAGTGACATGTCCAGCATGAA 193
                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                    16 GCGGCGGCTGCTGATTGTGTTCTAGGGGACGGAGTAGGGG--AAGACGTTTGCTCTCCCG
                                                                                                                                                                                                                                  74 GAACAGCCTATCTCATTCCTTTCCGATTACCCGTGGCGGGGAGAGATCAGGGCGGCGG
                                                                                                                                                                                                                                                                                1 GTGGCGGCTGCTGATTGTGTTCTAAGGGGACGGAGTGGGGGTAAAGACGTTTGCTCTCCTG
                                                                    TCCCGAATATGATTATTTATTCAAGTTACTTCTGATTGGCGACTCAGGGGTTGGAAAGTC 253
                                                                                                                                                                                                                GAACAGCCTATCTCATTCCCTTCGACTACCCGTGGCGCGGAGAGTCAGGGCGGCGG
TTGCCTTCTTAGGTTTGCAGATGATACATATACAGAAAGCTACATCAGCACAAT
                                  TTGCCTTCTTAGGTTTGCAGATGATACATATACAGAAAGCTACATCAGCACAAT
                                                                                                                                           CTGCAGCAGCAAGGGCGGCGGTGGCGGCGGCGGCAGCTGCAGTGACATGTCCAGCATGAA
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                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 7.4e-36;
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                                                                                                                                                                                                                                                                                                                                                      14;
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Search completed: June 22, 2003, 22:38:01 Job time: 228 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
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Perfect score:
Sequence:
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                                                                                                                                                                                                                           Score
         768.5
768.5
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683
637
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1: SIDS2/gcgdata/genesed/geneseqp-embl/AA1980.DAT:*

2: SIDS2/gcgdata/genesed/geneseqp-embl/AA1981.DAT:*

3: SIDS2/gcgdata/genesed/geneseqp-embl/AA1982.DAT:*

4: SIDS2/gcgdata/genesed-geneseqp-embl/AA1983.DAT:*

5: SIDS2/gcgdata/genesed-geneseqp-embl/AA1983.DAT:*

6: SIDS2/gcgdata/genesed-geneseqp-embl/AA1985.DAT:*

6: SIDS2/gcgdata/genesed-geneseqp-embl/AA198.DAT:*

7: SIDS2/gcgdata/genesed-geneseqp-embl/AA198.DAT:*

8: SIDS2/gcgdata/genesed-geneseqp-embl/AA198.DAT:*

9: SIDS2/gcgdata/genesed-geneseqp-embl/AA198.DAT:*

10: /SIDS2/gcgdata/genesed-geneseqp-embl/AA199.DAT:*

11: /SIDS2/gcgdata/genesed-geneseqp-embl/AA199.DAT:*

12: /SIDS2/gcgdata/genesed-geneseqp-embl/AA199.DAT:*

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Query
Match
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Gapop 10.0 , Gapext 0.5
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886
1 MSSMNPEYDYLFKLLLIGDS.....EKSNYKIQSTPVKQSGGGCC 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                         Length
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    AAB34844
AAB34816
AAAB34816
AAA013525
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AAB58024
AAY00919
AAU28024
ABB59808
AAG07763
AAG10858
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Gene 44 human secr
Human secreted pro
Human secreted pro
Human polypeptide
Breast and ovarian
Human Rab protein,
Novel human secret
Drosophila melanog
Arabidopsis thalia
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	AAB09981	21	199	43.7	387	Ü
Human Rab10 prote		21	199	43.7	387	4
Lung cancer		21	246	44.1	390.5	w
Novel human		22	209		390.5	N
Drosophila me		22	204	44.4	393	-
Canine Rabic		21	201	44.4	393	0
Novel human	ABG07266	22	218	45.1	399.5	ø
		21	141	•	400	80
Arabidopsis		21	130	•	403	7
Human prostate		21	218	45.5	403.5	9
Human protein seq		22	200	•	403.5	Ü
Human Rab10		21	200	•	403.5	4
Amino acid sequen		21	200	•	403.5	ω̈
		21	163		405	Ñ
Drosop		22	207	•	408	Ĥ
Novel		22	335		409.5	0
. Human		22	207		414	ø
Amino		22	207		414	æ
Human		23	221		417	7
Human		22	213	47.3	419	9
Arabidopsis		21	254		428.5	ū
Arabidopsis		21	253	48.4	428.5	4
Arabidopsis		21	216		428.5	ũ
Arabidopsis		21	216		428.5	Ñ
Arabidopsis		21	234	48.5	429.5	μ
Arabidopsis thali		21	224		429.5	Ö
Zea mays protein		21	215		431	٥
Arabidopsis		21	216		442	8
		21	218		444	7
Arabidopsis	AAG4882	21	197	65.5	580	6
		21	254		612	Ġ
Arabidopsis		21	221		612	4
Arabidopsis t		21	218		612	w
Arabidopsis	AAG3049	21	203	69.8	618.5	N
	AAG30498	21	258		619.5	-

ALIGNMENTS

RESULT 1	
TAN S	TI STORES TO THE STATE OF THE
×ŧ	Andidato, Floceil, 200 AA.
ΑC	AAB34843;
X	
X DI	26-JAN-2001 (first entry)
BG	Gene 44 human secreted protein homologous amino acid sequence #131.
XX	
KW.	<pre>Human; secreted protein; diagnosis; cytostatic; immunosuppressive;</pre>
KW	nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
ΚW	antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW	<pre>antibacterial; antifungal; antiparasitic; cardiant; gene therapy;</pre>
KW	<pre>cancer; immune disorder; cardiovascular disorder; wound healing;</pre>
×	Hedrorogical disease; Infectious disease; Chromosome identification.
S	Homo saniens
××	
PN	WO200058356-A1.
×	
PD	05-0CT-2000.
o X	22-WAR-2000. 2000WO-MC07535
×	
PR	26-MAR-1999; 99US-0126511.
Y PR	17-DEC-1999; 99US-0172413.
PA	(HUMA-) HUMAN GENOME SCI INC.
×	
PI	Rosen CA, Ruben SM, Komatsoulis G;
×	

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RESULT 2
AAB34844
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiallergic; hepatotropic; antidiabetic; antiliflammatory; antiulce: vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant. The polynucleotides and polypeptides are useful for preventing, treating or ameliorating a medical condition in e.g. hums mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The polynucleotides are useful for chromosome identification. They are also useful as probes diagnosing a disorder related to the female reproductive system, particularly breast and/or ovary cancer. They are also useful in the
                                                                    antibacterial; antifungal; antiparasitic; cardiant; gene therapy
cancer; immune disorder; cardiovascular disorder; wound healing;
                 Homo sapiens.
                                                                                                                        Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis, treatment and prevention of cancer, immune disorders, cardiovascular disorders, wound healing, neurological diseases and infectious disease. AAC59957 to AAC59965 and AAB34772 represents sused in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              particularly breast and/or ovary cancer. They are also useful in the gene therapy of breast and ovarian cancer. Nucleic acids, protein, antibodies, agonists and antagonists from the present invention are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and cells the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rifty nucleic acid molecules encoding human secreted proteins, in the prevention, treatment and diagnosis of cancer, immune d
                                                     neurological disease;
                                                                                                            antidiabetic;
                                                                                                                                                                                                                                                                                                AAB34844 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homologous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 415-416; 425pp; English.
                                                                                                                                                                                                                       26-JAN-2001
                                                                                                                                                                                                                                                              AAB34844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide sequences given in AAC59966 to AAC60015 encode in secreted proteins given in AAB34773 to AAB34822. AAB34823 to
                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                            149
                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                   secreted
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                                                                                                                                                                                                                                                                                                                                                                                                           TAGGAEKSNYKIQSTPYKQSGGGCC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSSMNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSEMTMAAEIKKRMGPGA
                                                                                                                                                                                                                                                                                                                                                                                      TAGGAEKSNYKIQSTPVKQSGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLQEIDRYASENVNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLQI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSSMNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apresent human secreted polypeptide sequences and proteins to them, which are given in the exemplification of the present Human secreted proteins have activities based on the tissues the genes are expressed in examples of activities include:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive; nootropic; neuroprotective; antiviral; c; hepatotropic; antidiabetic; antiinflammatory; antiulcer; anticonvulgant; antibacterial; antifungal; antiparasitic; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                     (first entry)
                                                                                                            antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,
                                                                                                                                                                                 protein sequence encoded by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders
                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.1%;
84.4%;
                                                     infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                205
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                                                                                                                                                                                                                                                                                              ₹
                                                                                                         antiulcer;
                                                   disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
.6e-79;
                                                   chromosome
                                                                                                         vulnerary; anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ESFNNVKQWLQEIDRYASENVNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                     gene therapy;
                                                   identification
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                                                                                                                                                                                 NO:132.
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RESULT 3
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AAB34816 standard; Protein;

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Best Local S
Matches 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The polynucleotides are useful for chromosome identification. They are also useful as probes for diagnosing a disorder related to the female reproductive system, particularly breast and/or ovary cancer. They are also useful in the gene therapy of breast and ovarian cancer. Nucleic acids, protein, antibodies, agonists and antagonists from the present invention are useful in the diagnosis, treatment and prevention of cancer, immune disorders, cardiovascular disorders, wound healing, neurological diseases and infectious disease. AAC59957 to AAC59955 and AAB34772 represents sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human secreted proteins given in AAB34773 to AAB34822. AAB34823 to AAB34852 represent human secreted polypeptide sequences and proteins AAB34852 represent human secreted polypeptide sequences and proteins no fine present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in Examples of activities include: cytostatic; immunosuppressive; nootropic; neuroprotective; antivital; antiallergic; hepatotropic; antidiabetic; antilalergic; hepatotropic; antidiabetic; antiferance; antilalergic and antiallergic proteins antiallergic antidiabetic antidiabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; and cardiant. The polynucleotides and polypeptides are useful for preventing, treating or ameliorating a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 416-417; 425pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular disorders and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-594639/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1999;
17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide sequences given
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                                                149
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                             TAGGAEKSNVKIQSTPVKQSGGGCC
                                                                                                                                                                                                                                                                                                                                      MSSMNPEYDYLFKLLLIGDSGYGKSCLLLRFADDTYTESYISTIGYDFKIRTIELDGKTI
TAGGAEKSNVKIQSTPVKQSGGCC
                                                                                                     LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGA
                                                                                                                             LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGA 148
                                                                                                                                                                                                        KLQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLQEIDRYASENVNKL
                                                                                                                                                                                                                                                                                                         Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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99US-0172413.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 860; DE Pred. No. 7.66 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding human secreted | and diagnosis of cancer, neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present
205
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
.6e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
                                                                                                                                                                                                                                                         ESFNNVKQWLQEIDRYASENVNKL
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                                                                                                                                                                                                                                             The polynucleotide sequences given in AAC59966 to AAC60015 encode the Chaman secreted proteins 1 to AAB34822. AAB34823 to AAB34823 represent human secreted polypeptide sequences and proteins CC AAB34827 represent human secreted polypeptide sequences and proteins CC invention. Human secreted proteins have activities based on the tissues CC and cells the genes are expressed in Examples of activities include: CC cytostatic; immunosuppressive; noctropic; neuroprotective; antivital; cc antiallergic; hepatotropic; antidiabetic; antifungal; antiparastic; and CC cardiant. The polynucleotides and polypeptides are useful for CC preventing, treating or ameliorating a medical condition in e.g. humans, CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The CC increase or decrease storage capabilities. The polynucleotides are useful for CC useful for chromosome identification. They are also useful as probes for CC useful for chromosome identification. They are also useful in the gene CC therapy of breast and/or ovary cancer. They are also useful in the gene CC therapy of breast and/or ovary cancer. They are also useful in the gene CC tharpay of breast and ovarian cancer. Nucleic actids, protein, antibodies, CC agonists and antagonists from the present invention are useful in the CC diagnosis, treatment and prevention of cancer, immune disorders, cardiovascular disorders, wound healing, neurological diseases and CC used in the exemplification of the present invention.
                                                                                                                                               Query Match
Best Local S
Matches 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and disquosis of cancer, immune disorders cardiovascular disorders and neurological diseases .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; diagnosis; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatorropic; antidiabetic; antifilammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune 'disorder; cardiovascular disorder; wound healing; neurological disease; infectious disease; chromosome identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 393-394; 425pp; English.
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                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-1999;
17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-2000;
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                                                                                                                                                  165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted protein sequence encoded by gene 44 SEQ ID
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                                     65
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                                                                                                                                                                   Similarity
                                                                 DYLFKLLLIGDSGYGKSCLLLRFADDTYTESYISTIGYDFKIRTIELDGKTIKLQI---- 64
GOERFRIITSSYYRGAHGIIVVYDVTDQESFNNVKQHQELDRYASENVKLLVGNKCDL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM,
                                                                                                                                                                                                                       198 AA;
                                                                                                                                                  Conservative
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99US-0172413.
                                                                                                                                                               92.2%;
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                                                                                                                                           Score 817; DB 21;
Pred. No. 1.6e-74;
0; Mismatches 0;
                                                                                                                                             0;
                                                                                                                                                                              Length 198;
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RESULT 4
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                                                                                                                   Query Match
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Matches 156
                                                                                                                                                                                                                                                                                                                                                                The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoliesis regulating activity, tissue growth factor activity, haematopoliesis regulating activity, tissue growth factor activity. Immunomodulatory activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 27417; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAI93456
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18-MAY-2000;
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                                                                                                                                                                                                                                Sequence
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                221
                                                                                                                      Conservative
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2000US-0577409.
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                                                                                                            Score 768.5; DB 3
Pred. No. 1.5e-69;
8; Mismatches
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                                                                                                                                                                        22;
                                                                                                                Indels 33;
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RESULT 5
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                       antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease,
                                                                                                                   proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the invention and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; neuroprotective; antiviral; antiallergic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
            allergies,
                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W0200055173-A1
                                                                                                                                                                                                            proteins AAB58711
                                                                                                                                                                                                                              Sequences AAF21614 -
                                                                                                                                                                                                                                                                                                      treatment
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; breast cancer; ovarian cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB58758 standard;
                                                                                                                                                                                                                                                                                                                      polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                            ( HUMA - )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79
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                                                                                                                                                                                                                                                                                                                                                                  AAF21661
                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN GENOME
   mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               гот----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGG-ERPNLKIDSTPVKPAGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGAEKSNVKIQSTPVKQSGGGCC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGNKSDLTTKKVVDNTTAKEFADSLGIPFLETSAKNATNVEQAFMTMAAEIKKRMGPGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLL
                                                                                                                                                                                                                                                                                      breast and ovarian cancer associated gene des encoded by these genes, useful in the pand diagnosis of cancer, immune disorders, and neurological diseases
                                                                                                                                                                                                                                                            Page
               autoimmune haemolytic
                                                                                                                                                                                                                                                                                                                                                                                                              Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurpprotective; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-US05881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                        895-896; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder; wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                             MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                           AAF22031 represent DNA sequences encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                            SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         associated antigen protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
              anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221
multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiallergic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s; ulcerative colitis; neurological disease.
            autoimmune thyroiditis,
                                                                                                                                                                                                                                                                                                      disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -ESFNNVKQWLQEIDRYASENVNKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosuppressive;
                                                                                                                                                                                                                                                                                                                 prevention,
                                                                                                                                                                                                                                                                                                      cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anticonvulsant;
                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                             New purified human Rab proteins treating e.g. AIDS, immunodefic cancer, inflammation or autoimmu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis and ulcerative colitis; cardiovascular disorders such myocardial ischaemias; wound healing; neurological diseases such cerebral anoxia and epilepsy; and infectious diseases.
                                                                                                                                  N-PSDB;
                                                                                                                                                                            (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                              17-AUG-1998;
                                                                                                                                                                                                                                25-FEB-1999.
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                           neurodegenerative
                                                                                                                                                                                                                                                                                                           Rab protein;
                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                              28-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                AAY00919;
                                                                                                                                                                                                                                                                                                                                                                                AAY00919
                                                                                                                                                                                                                                                                                                                                                                                         ნი
                                                                                                                                          1999-181042/15.
                                                                                                                                                                                                                                                                                                    differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            142
                                                                                                                                                                                                                                                                                                                                                                                                                          202
                                                                                                                                                                                                                                                                                                                                                                                                                                          150
                                                                                                                                                                                                                                                                                                                             Rab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
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                                                                                                                                                           NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
                                                                                                                                  AAX27232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                         SGG-ERPNLKIDSTPVKPAGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSEMTMAAEIKKRMGPGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSMNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAEKSNVKIQSTPVKQSGGGCC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGNKSDLTTKKVVDNTTAKEFADSLGIPFLETSAKNATNVEQAFMTMAAEIKKRMGPGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQI-----ESFNNVKQWLQEIDRYASENVNKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAMNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLL
                                                                                                                                                                                                                                                                                                                            protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 AA;
                                                                                                                                                          Hillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                            RABP-1; RABP-2;
                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                             970S-0916901
                                                                                                                                                                                                              98WO-US16983
                                                                                                                                                                                                                                                                                           disease;
                                                                                                immunodeficiencies,
                                                                                                                                                                                                                                                                                                                           RABP-2,
                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.5%;
                                                                                                                                                                                                                                                                                                  apoptosis;
                                                                                                                                                           Lal
                                                                                                                                                                                                                                                                                          myelodysplastic syndrome; wasting
                                                                                                                                                                                                                                                                                                                            protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 768.5;
Pred. No. 1.5e
8; Mismatches
                                                                                                                                                                                                                                                                                                           RABP-3; human;
                                                                                                                                                           Ψ.
                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                 genetic
                                                                                                                                                                                                                                                                                                                                                                                                                          224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         768.5; DB 2
                                                                                                                                                                                                                                                                                defect; diagnosis;
                                                                                                                                                                                                                                                                                                           vesicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                           trafficking;
                                                                                                                                                                                                                                                                                                 proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such
                                                                                                                                                                                                                                                                                therapy.
                                                                                                                                                                                                                                                                                          disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149
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This sequence is a human Rab protein of the invention, designated RABP-2. The Rab proteins, RABP-1, RABP-2 and RABP-3 are involved invesicle trafflicking, cell function, and cell differentiation. The polypeptides, DNAs and agonists can be used to prevent or treat a disorder associated with an increase in apoptosis, e.g. infectious

Claim

23;

Fig 2;

94pp; English.

or autoimmune

diseases

to develop products neurodegenerative di

diseases,

for

disorder associated with an increase in apoptosis, e.g. infect genetic immunodeficiencies, neurodegenerative diseases such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral

degeneration,

myelodysplastic

infectious

RABP

as

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RESULT 7
AAU28024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc syndromes such as aplastic anaemia, ischaemic injuries such as myocardial criticals, stroke, and reperfusion injury, toxin-induced diseases such cc as alcohol-induced liver damage, cirrhosis, and lathyrism, wasting cd diseases such as cachexia, viral infections, and osteoporosis. They can cc also be used to stimulate cell proliferation for use in transplantation co or to produce cells to fight an infection or a cancer or to correct a cc genetic defect in a disease such as sickle cell beta thalassemia, cystic clibrosis or Huntington's chorea. Antagonists can be used to prevent or cc treat a disorder associated with cell proliferation e.g. cancers or cc treat a disorder associated with cell proliferation e.g. cancers or cc treat a disorder associated with cell proliferation e.g. cancers or cc treat a disorder associated with cell proliferation e.g. cancers or cc treat a disorder associated with cell proliferation e.g. cancers or cc treat a disorder associated with cell proliferation e.g. cancers or cc treat a disorder associated with cell proliferation e.g. cancers or cc treat a disorder associated with cell proliferation e.g. cancers or cc treat a disorder associated with cell proliferation e.g. cancers or cc treat a disorder associated with cell proliferation e.g. cholecystitus, cholecystitus, coloreystitus, coloreys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 156; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                       Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
                                                           05-MAR-2001; 2001WO-US04942.
                                                                                                                                                      WO200166689-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU28024 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                            fertility; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAEKSNVKIQSTPVKQSGGGCC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MNPEYDYLFKLLLIGDSGYGKSCLLLRFADDTYTESYISTIGYDFKIRTIELDGKTIKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-ERPNIKIDSTPVKPAGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKSDLTTKKVVDNTTAKEFADSLGIPFLETSAKNATNVEQAFMTMAAEIKKRMGPGAASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I-----ESFNNVKQWLQEIDRYASENVNKLLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            secretory protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
2000US-0519705
2000US-0574454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.5%;
77.2%;
                                                                                                                                                                                                                                          pain;
                                                                                                                                                                                                                                          antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 766.5;
Pred. No. 2.1e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq ID No 193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                766.5;
No. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 2v,
2.1e-69;
7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
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121

NKSDLTTKKVVDNTTAKEFADSLGIPFLETSAKNATNVEQAFMTMAAEIKKRMGPGAASG

60 91 120 151

IMDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESYANVKQMLQEIDRYASENVNKLLVG
NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG

-----ESFNNVKQWLQEIDRYASENVNKLLVG

MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ

GAEKSNYKIQSTPVKQSGGGCC

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δĀ
                                                                                                               The invention relates to novel isolated human secreted polypeptides (I) cand polynucleotides (II). (I) and (II) are useful for treating confilmentary conditions such as arthritis, nephritis, cronn's disease, considered in increasing haematopolesis, mephritis, cronn's disease, and is involved in increasing haematopolesis, stem cell survival, bone growth can remodeling (I) (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides.

C(I) induces the proliferation of neural cells and regeneration of nerve can brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, can artivity, regulation of hæmatopolesis and is useful for treating myeloid cor lymphoid cell disorders, platelet disorders unch as thromborytopenia culcers, for treating osteoprosis, osteoarthritis, bone degenerative culcers, for treating osteoprosis, osteoarthritis, bone degenerative culcers, for treating osteoprosis, osteoarthritis, bone degeneration of disorders uncluding severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple scierosis, creations and conditions, such as asthma or other respiratory problems. Cc reactions and conditions, such as asthma or other respiratory problems. Cc fertility, metabolism, catabolism, anabolism, storage or elimination of distance effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an combined immunographic consistion of the invention.
                                                 Matches
                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
20-OCT-2000;
                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polypeptides and prepared from various cancer, neurological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; SEQ ID No 193; 107pp; English.
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                                               156;
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                                                            Similarity
MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
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2000US-0616847.
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                                               Conservative
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Drmanac
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                                                            86.5%;
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Pred. No. 2.1e-69;
6; Mismatches 7;
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Zhang
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ng J, Chen
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RESULT 8
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Best Local S
Matches 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABL0101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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N-PSDB; ABL03911.
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11-JUL-2000;
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Pred. No. 6e-61;
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NKCDLTTKKYVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG	IESFNNVKQ 	MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTTELDGKTIKLQ 	; Score 637; DB 21; ; Pred. No. 2.6e-56; 11; Mismatches 25;		P.0.55 & 0.86 7 P. &	-	ю И. й. д. б. а. б. б. б. б. а. а. с. б.	-
EQSFMTMAAEIKKRMGPGA:	ESFNNVKQWLQEIDRYASENVNKLLVG 	STIGVDFKIRTIELDGKTII STIGVDFKIRTVEQDGKTII	Length 202; ; Indels 34; Gaps					
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SULT 10 G10858 AAG10858 standard; Prot AAG10858; 17-OCT-2000 (first ent Arabidopsis thaliana pr Protein identification assay; ge termination sequence. Arabidopsis thaliana. EP1033405-A2. 06-SEP-2000; 2000EP-030 25-FEB-1999; 99US-011 05-MAR-1999; 99US-011 06-APR-1999; 99US-011 19-APR-1999; 99US-011 19-APR-1999; 99US-011 19-APR-1999; 99US-011 10-APR-1999; 99US-011 11-MAY-1999; 99US-011 23-APR-1999; 99US-011 23-APR-1999; 99US-011 23-APR-1999; 99US-011 23-APR-1999; 99US-011 23-APR-1999; 99US-011 23-APR-1999; 99US-013 30-APR-1999; 99US-013 31-MAY-1999; 99US-013 31-JUN-1999; 99US-013	-	77	-			į	1	;
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150 GARSHWYLINSPYNYQSGOODC 173 180 GSEPPYNQSGOODC 173		י גע				9908-0138540.		PR:
152 GARSHWICHSTPWINGSCROCC 173 180 GSEPPTUJANGOPWAG-SCC 200 SULT 10 MAGIDDS standard: Protein; 202 AA. AAGIDDS standard: Protein; 202 AA. AAGIDS standard: Protein; 202 A		ָ ק				9975-0138094		B :
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152 CAREANNY CONTYPOGROCOCC 173 160 GSEPPTOLEGOPYMOD-SGCC 2000 STUZT 10 181 - 111 - 111 111		ğ				99US-0137528.		PR
152 CARSENVICTORIVANCO-SCCC 200 18:		PR				99US-0137222.	01-JUN-1999;	PR
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152 CARRANKYCGETYPOGROCCC 173 180 GSEPPYOLEOGYMOD-SGCC 200 SULT 10 CARGES CARGES ANGIOSS:	••	PR				99US-0136392.	2/-MAY-1999;	77
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152 CARRESONVELOGRAPHO-SOCC 200 152 CARRESONVELOGRAPHO-SOCC 200 153 LINE	•	P				99US-0135353.	21-MAY-1999;	PR
122 GARSSWAYCISTOPHUNOC-SGCC 200 123 123 GARSSWAYCISTOPHUNOC-SGCC 200 124 125 1111 111 111 111 111 111 111 111 11		PR				990S-0135124.	20-MAY-1999;	אַקי
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122 GARSENNYLOGOPHYNOC-SGCC 200 123 (1::	٠.	בא				9905-0154256.	11 -MAI - 1999;	;
122 GERENNYOU FORCE 200 123 (1:	-	77			•	0000 0104000.	11-WAY-1000.	3;
122 GARKINNYLOSPPYVQG-SGCC 200 123 GSKPPTYQIRGQPYWQG-SGCC 200 224 11		7 ;				99115-0132863	07-MAY-1999	PR
122 GARKSNWIGSTPWOGO-SCCC 200 123 G::::::::::::::::::::::::::::::::::::	•	PR :			•	99US-0132487.	06-MAY-1999;	PR
123 GAKKNWICKOSPPVNQC-SGCC 200 180 GSKPPTVQIRGQPVNQC-SGCC 200 180 GSKPPTVQIRGQPVNQC-SGCC 200 281 B.JUN-1999 1858; standard; Protein; 202 AA. 282 B.JUN-1999 1858; standard; Protein; 202 AA. 283 B.S. standard; Protein; 202 AA. 284 B.JUN-1999 1858; standard; Protein; 202 AA. 285 B.S. standard; Protein; 202 AA. 286 B.S. standard; Protein; 202 AA. 286 B.S. standard; Protein; 202 AA. 287 B.S. standard; Protein; 202 AA. 287 B.S. standard; Protein; 202 AA. 288 B.S. standard; Protein;	٠.	PR				99US-0132486.	06-MAY-1999;	PR
152 GARKSNYKIOSPPVRQC-SGCC 173 152 (1: - - - - - - - - - - - - -	•	РR				9905-0132485.	05 MAI - 1999;	7
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|:|: || || || || 204 TVQIRGQPVNQQ-SGCC 219
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990S-0161406

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990S-0161360

990S-0161361

990S-0161361

990S-0161920

990S-0161993

990S-0161993
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Coatch completed: Tues 10 2002 15 21 00	237 TVQIRGQPVNQQ-SGCC	Ov 157 NVKIOSTPVKOSGGGCC 173	Db 178 TSQKVVSTETAKAFADELGIPFLETSAKNATNVEEAFMAMTAAIKTRMA-SQPAGGSKPP 236	DYT:	Db 118 GQERFRTITSSYYRGAHGIIVTYDVTDLESFNNVKQWLNEIDRYASENVNKLLVGNKCDL	Qy 65ESFNNVKC	Db 58 DYLFKLLLIGDSGYGKSCLLLRFADDSYLDSYISTIGYDFKIRTVEQDGKTIKLQIWDTA	Qy 9 DYLFKLLLIGDSGYGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQI	Matches 128; Conservative 11; Mismatches 24	69.18;	 28-OCT-1999;	PR 26-OCT-1999; 99US-0161361.	26-OCT-1999;	26-OCT-1999;	25-OCT-1999;	PR 25-0CT-1999; 99US-0161404.	`	22-OCT-1999;	22-OCT-1999;	PR 21-OCT-1999; 99US-0160815.	PR 21-OCT-1999; 99US-0160814.
			EEAFMAMTAAIKTRMA-SQPAGGSKPP 236	QSFMTMAAEIKKRMGPGATAGGAEKS 156	SFNNVKQWLNEIDRYASENVNKLLVGNKCDL 177	ESFUNVKQWLQEIDRYASENVNKLLVGNKCDL 96	FIGVDFKIRTVEQDGKTIKLQIWDTA 117	TIGVDFKIRTIELDGKTIKLQI 64	24; Indels 34; Gaps 3;	21; Length 254;											

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Title: Perfect score: Sequence:

US-09-820-003B-2 886 1 MSSMNPEYDYLFKLLLIGDS......EKSNVKIQSTPVKQSGGGCC 173

Scoring table:

Searched: 283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

26 27 28 29	14 15 16 19 19 22 22 23 24	1 2 3 3 5 5 6 6 7 7 7 10 11 11 13	Result
572.5 571 523 468.5	631.5 627.5 623.5 619.5 618.5 618.5 613.5 613.5 598.5 590.5	860 860 840 849 812.5 771.5 773 671.6 658.5 646.5 646.5	Score
59.0 52.0		97.1 97.1 95.8 91.7 95.7 74.5 73.0 73.0	Query Match
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409.5	418	418	426.5	428.5	429.5	429.5	430.5	435.5	438.5	439.5	442	447	461
46.2	47.2	47.2	48.1	48.4	48.5	48.5	48.6	49.2	49.5	49.6	49.9	50.5	52.0
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ALIGNMENTS

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F;12-127/Domain: translation elongation factor Tu homology <ETU>
F;18-25/Region: nucleotide-binding motif A (P-loop)
F;62-67/Region: nucleotide-binding motif B
F;124-127/Region: GTP-binding NKXD motif
F;124-127/Region: GTP-binding SAK/L motif
F;154-156/Region: GTP-binding SAK/L motif
F;244.25,43,124,125,127,124/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, FF;194/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status pref;204,205/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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C; Superfamily:
C; Keywords: end
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C;Speckes: Canis lupus familiaris (dog)
C;Date: 19-Feb-1994 #sequence_revision
C;Accession: S19104; A36364; S15600
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C;Function:
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A; Residues: 1-157, 'EK', 160-205
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A;Title: Molecular cloning of YPTL/SEC4-related
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A; Residues: 1-205 <ZER>
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Best Local Similarity
Matches 173; Conserv
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ras transforming protein; translation elongation factor Tu homology
doplasmic reticulum; Golgi apparatus; GTP binding; lipoprotein; membrane p
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Pred. No. 2.2e-62;
0; Mismatches 0
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                                                                                                                                                       GTP-binding protein Rabl - rat
N;Alternate names: transforming protein ypt1 homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Aug-1992 #sequence_revision 06-Dec-1996 #
                                                                                 R;Touchot, N.; Chardin, P.; T. Proc. Natl. Acad. Sci. U.S.A. A;Title: Four additional members.
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         A; Molecule type: mRNA
A; Residues: 1-205 < TO
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A; Introns: 8/2; 32/3; 64/3; 96/3; 140/3
C; Function: 8/2; 32/3; 64/3; 96/3; 140/3
C; Function: probably involved in protein transport from the endoplasmic recommendation: probably involved in protein; translation elongation factor Tu how c; Superfamily: ras transforming protein; translation elongation factor Tu homology <ETU>
C; Keywords: endoplasmic reticulum; Golgi apparatus; GTP binding; lipoprotein tein
F; 127/Domain: translation elongation factor Tu homology <ETU>
F; 18-25/Region: nucleotide-binding motif A (P-loop)
F; 62-67/Region: nucleotide-binding motif B
F; 124-127/Region: GTP-binding MKXD motif F; 154-127/Region: GTP-binding MKXD motif F; 154-156/Region: GTP-binding SAK/L motif
F; 134, 25, 43, 124, 125, 127, 154/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asf; 194/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
F; 204, 205/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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A;Reference number: S06285; h
A;Accession: S06285
A;Molecule type: mRNA
A;Residues: 1-205 <HAU>
C;Genetics:
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A;Title: Nucleotide sequence of the mouse ypt1 gene encoding A;Reference number: S05551; MUID:89386011; PMID:2306528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Haubruck, H.; Disela, C.; Wagner, EMBO J. 6, 4049-4053, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X15744; NID:g55458; PIDN R;Haubruck, H.; Disela, C.; Wagner, P.; Gallwitz,
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Best Local S
Matches 173
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names: GTP-binding
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                       TAGGAEKSNVKIQSTPVKQSGGGCC
                                                                                                                         LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSEMTMAAEIKKRMGPGA
                                                                                                                                                                                                                                                                                                                         MSSMNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTI
                                                                                              LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGA
                                                                                                                                                                                                   KLQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLQEIDRYASENVNKL
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84.4%;
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Pred. No. 2.2e-62;
0; Mismatches 0;
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tus predicted
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RESULT 5
D38625
D38626
G7P-binding protein o-rabl - electric ray (Discopyge ommata)
G7P-binding protein o-rabl - electric ray (Discopyge ommata)
G7P-binding protein o-rabl - electric ray (Discopyge ommata)
G7P-binding protein 23-Aug-1991 #text_change 02-Feb-2001
G7Accession: D38625
A7Title: A family of ras-like G7P-binding proteins expressed in electromotic Argerian and Argerian and
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A;Description: probably involved in protein transport from the endoplasmic reticulum that A;Description: probably involved in protein; translation elongation factor Tu homology C;Roywords: endoplasmic reticulum; Golgi apparatus; GTP binding; lipoprotein; membrane fill-127/Domain: translation elongation factor Tu homology <ETU> F;12-127/Domain: translation elongation factor Tu homology <ETU> F;18-25/Region: nucleotide-binding motif A (P-loop)
F;62-67/Region: nucleotide-binding motif F:124-127/Region: GTP-binding MXXD motif
F:124-127/Region: GTP-binding NXXD motif
F:134-156/Region: GTP-binding NXXD motif
F:134-157/Region: GTP-binding sak/L motif
F:134-157/Region: GTP-binding site: Mg-GTP (Lys, Ser, Thr. Asn, Lys, Asp, Ser) #sta
F:194/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
F:204/205/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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Similarity 81.2%;
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NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG
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                                                                                       IWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLQEIDRYASENVNKLLVG
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Pred. No. 1.5e-58;
3; Mismatches 2;
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Pred. No. 1.7e-61;
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RESULT 7

$38339
GTP-binding protein rabl - great pond snail
GTS-becies: Lymnaea stagnalis (great pond snail)
C;Species: Lymnaea stagnalis (great pond snail)
C;Accession: $38339; $32206
A;Title: Isolation and characterization of three cDNAs coding for Rab prote
A;Reference number: $38339; MUID:94039042; PMID:8223561
A;Accession: $38339
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$96147'
STP-binding protein rablB - rat
GTP-binding protein rablB - rat
Whaternate names: ras-related protein rablB
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
C;Accession: S06147; S03189
R;Touchot, N.; Zahraoui, A.; Vielh, E.; Tavitian, A.
FEBS Lett. 256, 79-84, 1989
R;Title: Biochemical properties of the YPT-related rablB protein
A;Reference number: S06147; MUID:90033316; PMID:2509243
A;Accession: S06147
A;Accession: S06147
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Mucleic Acids Res. 17, 1770, 1989
A;Title: Nucleotide sequence of a rat cDNA:
A;Reference number: S03189; MUID:89160341; P
A;Accession: S03189
A;Molecule type: mRNA
A;Residues: 1-95,'YA',98-201
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A; Residues: 1-201 <TO
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                                                                                                                                                                                                                                                                                  G-ERPNLKIDSTPVKSASGGCC
                                                                                                                                                                                                                                                                                                                                                                   NKSDLTTKKVVDNTTAKEFADSLGVPFLETSAKNATNVEQAFMTMAAEIKKRMGPGAASG
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77.2%;
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Pred. No. 3e-5
6; Mismatches
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3e-55;
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Biosci. Biotechnol. Biochem. 62, 1885-1891, 1998
A, Title: Molecular cloning of cDNA for Brab from the brain of Bomby A, Reference number: JE0318; MUID:99053143; PMID:9836423
A; Accession: JE0318
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-202 <UNO>
A; Cross references: GB.AF013572
C; Superfamily: ras transforming protein; translation elongation fac C; Superfamily: ras transforming protein; translation elongation fac C; Reywords: GTP binding; nucleotide binding; P-loop
F; 9-124/Domain: translation elongation factor Tu homology <ETU>F; 121-124/Region: GTP-binding NKXD motif
F; 121-137/Region: GTP-binding SAK/L motif
F; 21, 22, 40, 121, 122, 124, 151/Binding site: Mg-GTP (Lys, Ser, Thr, Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Bombyx
C; Date: 05-Feb-199
C; Accession: JE031
R; Uno, T.; Ueno, N
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C; Superfamily: ras transforming protein; translation elongation factor Tu homology C; Superfamily: ras transforming protein; nucleotide binding; P-loop; prenylated cystel F; 12-127/Domain: translation elongation factor Tu homology <ETU>
F; 18-25/Region: nucleotide-binding motif A (P-loop)

F; 124-127/Region: GTP-binding MXXD motif F; 154-156/Region: GTP-binding SAK/L motif F; 154-156/Region: GTP-binding SAK/L motif F; 24, 25, 43, 124, 125, 127, 154/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser F; 24, 25, 43, 124, 125, 127, 154/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser F; 204, 205/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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A;Molecule type: mrNA
A;Residues: 1-205 AAGT>
A;Cross-references: EMBL:X72688; NID:g288933; PIDN:CAA51233.1; PID:g288934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Bombyx mori (silkworm)
Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change
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Best Local :
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dombyx mori (silkworm)
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NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG
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                                                         IWDTAGQERFRTITSSYYRGAHGIIIVYDCTDQDSFSNVKQWLEEIDRYACDNVNKLLVG
                                                                                                                                   MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTVDLNGKTIKLQ
                                                                                                                                                     MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
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66.5%;
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A;Cross-references: GB:S51252; NID:g262045; PIDN:AAB24564.1; R;Schulte, U; Algn, V; Hohelsel, J.; Brandt, P.; Fartmann, submitted to the Protein Sequence Database, May 2000 A;Reference number: Z25022 A;Accession: T49787

PID:g262046 B.; Holland,

æ :

Nyakatu

chromosome

molecular

19-Jan-2001

A; Reference number: A; Accession: S30096

A; Status: not compared with conceptual translation

A; Residues: 1-203 <HEI> A; Molecule type: DNA

A; Molecule type: I A: Residues: 1-203 A; Accession: T49787 A; Status: preliminary

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GTP-binding protein ypt1 [similarity] - Neurospora crassa N;Alternate names: protein B9J10.240; ras-related protein ypt1 C;Species: Neurospora crassa C;Date: 30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change C;Accession: S30096; T49787 R;Heintz, K.; Plafenthal, T.; Russo, V.E.A. Mol. Gen. Genet. 235, 413-421, 1992
A;Title: The Ncypt1 gene from Neurospora crassa is located on ch A;Reference number: S30096; MUID:93101148; PMID:1361212
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A; Introns: 8/2; 48/3; 64/3; 96/3
C; Superfamily: ras transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid A;Reference number: 221407 A;Accession: T33781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C39F7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-Jan-2000
C;Accession: T33781
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A;Experimental source: strain Bristol N2; clone C391
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A; Residues: 1-20:
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Matches
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                                                                                                                                                                                                                                                                                 TAGGAEKSNVKIQ-STPVK-QSGGGCC
                                                                                                                                                                                                                                                                                                                   LVGNKCDLTAKRAVETQAAQDYAGQLGIPFLETSAKSSTNVEQAFLTMASEIKSRMGPVQ
                                                                                                                                                                                                                                                                                                                                    LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAAMNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTI
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66.2%;
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.2e-46;
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A;Introns: 5/1; 10/2; 29/2; 45/2; 61/2; 85/2; 137/2; 172/1
A;Introns: 5/1; 10/2; 29/2; 45/2; 61/2; 85/2; 137/2; 172/1
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Reywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop;
F;9-124/Domain: translation elongation factor Tu homology <ETU>
F;15-22/Region: nucleotide-binding motif A (P-loop)
F;37-45/Domain: effector #status predicted <EFF>
F;121-124/Region: GTP-binding NRXD motif
F;121-124/Region: GTP-binding SAK/L motif
F;21,22;40,121,122,124,151/Binding slte: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #static F;202,203/Binding slte: geranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTP-binding protein yptC1 - Chlamydomonas reinhardtii

# Alternate names: membrane vesicle transport protein yptC1; ras-like yptC1 protein; sma
C; Species: Chlamydomonas reinhardtii
C; Date: 21-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 02-Feb-2001
C; Accession: JC4105

# A: Dietmaisc, W.; Fabry, S.; Huber, H.; Schmitt, R.
Gene 158, 41-50, 1995
Gene 158, 41-50, 1995
A; Title: Analysis of a family of ypt genes and their products from Chlamydomonas reinhar
A; Reference number: JC4105; MUID:95309723; PMID:7789809

A; Accession: JC4105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-203 CDIE>
A;Cross-references: GB:U13168; NID:g806723; PIDN:AAA82727.1; PID:g806724
C:Comment: This protein plays an essential role in the regulation of intracellular memb)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 4/2; 45/3; 61/3; 137/3
C; Superfamily: ras transforming protein; translation elongation factor Tu homology
C; Supperfamily: ras transforming protein; nucleotide binding; P-loop; prenylated cysteine
F;9-124/Domain: translation elongation factor Tu homology <FTU>
F;15-127Region: nucleotide-binding motif A (P-loop)
F;151-124/Region: GTP-binding NKXD motif
F;151-153/Region: GTP-binding SAK/L motif
F;21,22,40,121,122,124,151/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #s
F;202,203/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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A;Experimental source: BAC clone B9J10; strain OR74A
C:Genetics:
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A; Introns: 4/2;
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                              4 MNPEYDYLFKLLLIGDSGYGKSCLLLREADDTYTESYISTIGVDFKIRTIELDGKTIKLQ 63
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                                                                                                                   h 73.0%;
Similarity 65.7%;
34; Conservative
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MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTVELDGKVIKLQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                       9,
                                                                                                                                           Score 646.5; DB 2
Pred. No. 3.9e-45;
                                                                                                                   Mismatches
                                                                                                                                                                          DB 2;
                                                                                                                   26;
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                                                                                                                                                                          Length 203;
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RESULT 13
7C1247
GTP-binding protein yptV1 - Volvox carteri
C:Species: Volvox carteri
C:Species: Volvox carteri
C:Species: Volvox carteri
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C:Accession: JC1247
R:Fabry, S:; Natz, N.; Huber, H.; Palme, K.; Jaenicke, L.; Schmitt, R.
Gene 118, 153-162, 1992
A:Title: The yptV1 gene encodes a small G-protein in the green alga Volvox carteri: G
A:Reference number: JC1247; MUID:92380499; PMID:1511889
A:Accession: JC1247
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A;Introns: 4/2; 45/3; 61/3; 94/1
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
F;9-124/Domain: translation elongation factor Tu homology <ETU>
A; Gene: yptV1
A; Introns: 5/2; 10/3; 29/3; 45/3; 61/3; 85/3; 137/3; 172/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ypt1-related protein 1 [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000
C;Date: 19-Jun-2000 #sequence_revision 09-Jun-2000 #text_change
                                                                                                          A;Cross-references: GB:M93438; NID:g170660; PIDN:AAA34255.1; PID:g170661
                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-203 <FAB>
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T50323
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A;Experimental source: strain 972h(-); cosmid c1703
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A; Residues: 1-203 <MCD>
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                                                                                 Genetics
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%; Pred. No. 3.9e-45;
16; Mismatches 23
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GTP-binding protein ypt1 - Phytophthora infestans W;Alternate names: monomeric GTP-binding protein C;Species: Phytophthora infestans (potato late blight agent) C;Date: 14-May-1997 #sequence_revision 18-Jul-1997 #text_cha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Chen, Y.; Roxby, R.
Gene 181, 89-94, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 5/2; 45/3; 61/3; 108/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-201 <CHE>
                                                                                                                                                                                                                                                                                                      Superfamily: ras transforming protein; translation elongation face; Reywords: GTP binding; membrane trafficking; nucleotide binding; 9-124/Domain: translation elongation factor Tu homology <ETU>;15-22/Region: nucleotide-binding motif A (P-loop);121-124/Region: GTP-binding MKXD motif;121-124/Region: GTP-binding SKXD motif;151-153/Region: GTP-binding SAK/L motif;151-153/Region: GTP-binding SAK/L motif;151-153/Region: GTP-binding SAK/L motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: ypt1
                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Superfamily: ras transforming protein; translation elongation factor Tu homology ;Reywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop; ;9-124/Domain: translation elongation factor Tu homology <ETU>;15-22/Region: nucleotide binding motif A (P-loop);40-45/Region: GTP binding #status predicted;50-68/Region: GTP binding #status predicted;50-68/Region: GTP binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB:U30474; NID:g940431; PIDN:AAB40355.1; PID:g940432
Comment: This protein is involved in vesicle transport between the end
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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147-153/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -126/Region: GTP binding *status predicted
-153/Region: GTP binding *status predicted
,203/Binding site: geranyl-geranyl (Cys) (covalent) *status predicted
                                                                                                                                                                                                                                                Local
       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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                                        92
                                                                             61
                                                                                                                  64
                                                                                                                                                                                                                               al Similarity
139; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
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                                                                                                                                               MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
NKSDLTAKRVVSTDAAKEFAESLGIEFLETSAKNAANVEKAFMMMAAQIKKRM---
                                  NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNPEYDYLFKLLLIGDSGYGKSCLLLRFADDTYTESYISTIGYDFKIRTIELDGKTIKLQ
                                                                       IWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLHEIDRYACENVNKLLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAGGAEKSNVKIQSTPVKQSGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKSDLTGKKVVDYQAAKAFADEIGIPFLETSAKNATNVEQAFNTMAAEIKNRMASQPVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKCDLTTKKYVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMIMAAEIKKRMG----PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLAEIDRYASENVNKLLYG
                                                                                                                                                                                                                                                                                                     ,122,124,151/Binding site: Mg-GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                              71.3%;
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                                                                                                                                                                                                                             8,
                                                                                                                                                                                                                                            Score 631.5; DB 2
Pred. No. 6.2e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 642.5; DB 2;
Pred. No. 8.2e-45;
Pred. No. 8.2e-45;
                                                                                                                                                                                                                           Mismatches
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                                                                                               ----ESFNNVKQWLQEIDRYASENVNKLLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ESFNNVKQWLQEIDRYASENVNKLLVG
                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                   (Lys,
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                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                              Length 201;
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                                                                                                                                                                                                                         Gaps
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F;121-124/Region: GTP-binding NKXD motif
F;151-153/Region: GTP-binding SAK/L motif
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X72212; NID:g311906; PIDN:CAA51011.1; PID:g311907 C;Superfamily: ras transforming protein; translation elongation factor Tu | C;Reywords: GTP binding; nucleotide binding; P-loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Napier, J.A.; Shewry, P.R. submitted to the EMBL Data I A; Reference number: S34253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Nicotiana
C; Date: 06-Jan-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule
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Best Local S
Matches 129
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                                                                                                                                                                                                                                                                                               Similarity
 SAKPPTVNIRGQPVTQS-GGCC
                                  GAEKSNVKIQSTPVKQSGGGCC 173
                                                                   NKSDLTANRVVSYETAKAFADEIGIPFLETSAKDATNVEQAFMAMTSAIKNRMASQPANN
                                                                                                  NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG
                                                                                                                                      IWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLSEIDRYASDGVNKILVG
                                                                                                                                                                                                      MNPEYDYLFKLLLIGDSGYGKSCLLLRFADDTYLESYISTIGVDFKIRTYEQDGKTIKLQ
                                                                                                                                                                                                                            MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAPKAGVKL -- TPGQQVPSNGGSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAEKSNVKIQSTPVKQ--SGGG--CC
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #sequence_revision
                                                                                                                                                                                                                                                                                             70.8%; Score 627.5; 63.9%; Pred. No. 1.:
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                                                                                                                                                                       ESFNNVKQWLQEIDRYASENVNKLLVG
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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rPro; IPR005225; Small_GTP.
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SM00175; RAB; 1.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY S
PHOSPHORYLATION (BY C)
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RESULT 2
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P05711;
01-NOV-1988
01-NOV-1988
                                           PRINTS; PRO0449; RASTRNSFRMNG.
SMART; SMO0175; RAB; 1.
TIGR00231; small_GTP; 1.
GTP-binding; Lipoprotein; Prenylation; Protein transport; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJUE-9126801; PubMed-1648736;
MEDIJUE-91296801; PubMed-1648736;
Khosravi-Far R., Lutz R.J., Cox A.D., Conroy L., Bour Sinensky M., Balch W.E., Buss J.E., Der C.J.;
*Isoprenoid modification of rab proteins terminating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Touchot N., Chardin P., Tavitian A.;
"Four additional members of the ras gene superfamily isolated by oligonucleotide strategy: molecular cloning of YPT-related cDNAs
                                                                                                                                       InterPro; IPR001806;
InterPro; IPR005225;
Pfam; PF00071; ras;
                                                                                                                                                                                                                                PIR; A36364; A36364.
PIR; A39963; A39963.
HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                      EMBL; J02998; AAA42006.1; -.
EMBL; X56384; CAB56775.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. use by non-profit institutions as 1 modified and this statement is not rem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a rat brain library.";
Proc. Natl. Acad. Sci. U.S.A.
Endoplasmic
NP_BIND
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GTPASE ACTIVITY
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                                                                                                                                                                                                             InterPro; IPR003579; GTPase_Rab.
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RESULT 3
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Matches 171
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01-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-9111590; PubMed-1899244;
Ngsee J.K., Elferink L.A., Scheller R.H.;
A family of ras-like GTP-binding proteins expressed in electromotor neurons page 15. Electromotor J. Biol. Chem. 266:2675-2680(1991).
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRRAMS; TIGR00231; Small_GTP; 1.
GTP-binding; Lipoprotein; Prenylation; Protein tr
NP_BIND 15
2 GTP (BY SIMILARITY).
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TRAFFIC (BY SIMILARITY).
1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea; Torpediniformes; Narcinoidei; Narcinidae; Discopyge.
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01-AUG-1991 (Rel. 19, Last sequence update)
01-CTT-1994 (Rel. 30, Last annotation update)
Ras-related protein ORAB-1.
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InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
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Best Local Similarity
Matches 165; Conserv
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#EDLINE-91296801; PubMed-1648736;

#EDLINE-91296801; PubMed-1648736;

Khosravi-Far R., Lutz R.J., Cox A.D., Conroy L., Bour Sinensky M., Balch W.E., Buss J.E., Der C.J.;

"Isoprenoid modification of rab proteins terminating motifs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1989
01-JUL-1989
01-OCT-1994
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P10536;
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-89160341; PubMed-2493636;
MEDLINE-89160341; PubMed-2493636;
Zahraoul A., Touchot N., Chardin P., Tavitian
"Nucleotide sequence of a rat cDNA: rablB, enc
related protein."
related protein."
Nucleic Acids Res. 17:1770-1770(1989).
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                                                                                                                                                                                                                                                         CHARACTERIZATION.
MEDLINE-90033316; PubMed-2509243;
                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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Lett. 256:79-84(1989).
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Pred. No. 4.2e-62;
3; Mismatches 2;
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GERANYL-GERANYL (BY SIMILARITY)

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PIR; ?
              Agterberg M., van Die I., Yang H., Andriessen J.A., van Tetering A., van den Eljoden D.H., Ploegh H.L.; "Isolation and characterization of three cDNAs coding for proteins from the albumen gland of the mollusc Lymnaea Eur. J. Biochem. 217:241-246(1993).

1 FUNCTION: PROBABLY REQUIRED FOR TRANSIT OF PROTEIN: THROUGH GOLGI COMPARTMENT (BY SIMILARITY).

1 SUBCELLULAR LOCATION: GOLGI COMPARTMENT (BY SIMILARITY).
                                                                                                                                                                                                        RAB1_LYMST
Q05974;
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                  Eukaryota; Metazoa;
Lymnaeidae; Lymnaea.
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SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; Sm
GTP-binding; Lipoprotei
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Pfam; PF00071;
                                                                                               MEDLINE-94039042;
                                                                                                                         NCBI_TaxID=6523;
                                                                                                                                                     Lymnaea stagnalis
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InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
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01-FEB-1994 (Rel. 28
16-OCT-2001 (Rel. 40
GTP-binding protein
YPT-1 OR B9J10.240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
DOMAIN
LIPID
SEQUENCE FROM N.A.
STRAIN-74-OR23-1A;
                                       MEDLINE=93101148; PubMed=1361212;
Heintz K., Palme K., Diefenthal T., Russo V.:
"The Ncypt1 gene from Neurospora crassa is 1
molecular cloning and structural analysis.";
Mol. Gen. Genet. 235:413-421(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There
use by non-profit institutions as long as
modified and this statement is not removed. U
                                                                                            SEQUENCE FROM N.A. MEDLINE-93101148;
                                                                                                                                     Sordariales; Sor
NCBI_TaxID-5141;
                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomy Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                               YPT1_NEUCR P33723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
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PIR; S38339; S38339.
HSSP; P05713; 3RAB.
                                                                                                                                                                              Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGR00231;
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152; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ب
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SM00175; RAB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                               LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLQEIDRYASENVNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLQI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSSMNPEYDYLFKLLLIGDSGYGKSCLLLRFADDTYTESYISTIGYDFKIRTIELDGKTI
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73.8%;
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                                                                                                                                                                                                                                               Created)
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
MW; D5E0BDDCBB4A26FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 733; DB Pred. No. 3.4e 7; Mismatches
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                               Pezizomycotina;
                                                                                                                                                                                                                                                                                                                                                                        173
                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                          203
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                                                                                                                                                                                                                     update)
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                                                                                                                                                                 Sordariomycetes;
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                                                                   chromosome
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Brandt

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Fartmann

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Best Local :
                                                                                                                                                                                     Chlamydomonas reinhardtii.
Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
6TP-binding protein YPTC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YPT1_CHLRE
Q39571;
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MEDLINE-95309723; PubMed-7789809; Dietmaier W., Fabry S., Huber H., Schmitt R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Interpro; IPR001806; Ras_trnsfrmng.
Interpro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S51252; AAB24564.1; -. EMBL; AL356324; CAB92031.1; -.
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-i-FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
                                                                                                                                                                                 NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - I - SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                  STRAIN-cw15;
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRAFFIC (BY
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; P01112; 1PLJ.
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SM00175; RAB; 1
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Lipoprotein; Prenylation; Protein transport.
15 22 GTP /RY STMTTART...
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (PROBABLE).

GERANYL-GERANYL.
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    RESULT
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Best Local S
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                                                                                                                                                                                                                                                                                                                     YPT1_SCHPO STANDARD; pF
p11620;
01-CCT-1989 (Rel. 12, Created)
01-AUG-1990 (Rel. 15, Last seque
15-JUN-2002 (Rel. 41, Last annot
Ras-related protein ypt1.
YPT1 OR SPBC1703.10.
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NP_BIND 15

NP_BIND 63

NP_BIND 121

DOMAIN 37

LIPID 202

LIPID 203

SEQUENCE 203 AA;
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SEQUENCE FROM N.A.
MEDLINE-90228338; PubMed-2328721;
Miyake S., Yamamoto M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of a family of ypt genes and their products from Chlamydomonas reinhardtil.";
Gene 158:41-50(1995).
-I- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP-binding;
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InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffens A., Cadieu E., Drean S., Cloux S., Lelaure V., Mortier S.,
RA Goffens A., Cadieu E., Drean S., Gloux S., Lelaure V., Mortier S.,
RA Goffens A., Cadieu E., Drean S., Gloux S., Lelaure V., Mortier S.,
RA Goffens A., Cadieu E., Drean S., Gloux S., Lelaure V., Mortier S.,
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"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                             use by non-profit institutions as long as modified and this statement is not removed. Usentitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                       Ptam;
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                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
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MEDLINE-89296485;
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Nucleotide sequence of a gene encoding
Schizosaccharomyces pombe.":
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SIMILARITY: TO RAS PROTEINS. BELONGS TO
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$10025; $10025.
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rPro; IPR001806; I
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rPF00071; ras; 1
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                                                                                                                                                                         X52099; CAA36319.1; -. X15082; CAA33192.1; -. AL136536; CAB66454.1;
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 TIGR00231;
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Armstrong J.;
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17:4373-4373(1989).
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-f. Nagariensis / HK10;
STRAINS-92380499; PubMed-1511889;
MEDLINE-92380499; PubMed-151889;
MEDLINE-92380499; PubMed-151889; PubMed-151889
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InterPro; IPR005225;
Pfam; PF00071; ras; ]
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01-JUL-1993
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Volvocaceae; Volvox.
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InterPro; IPR001806;
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HSSP; P05713; 3RAB.
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SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
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GTP (BY SIMILARITY).
EFFECTOR REGION (PROBABLE).
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No. 5.3
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Volvox
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01-NOV-1997 (1
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Ras-like GTP-L
                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                   EMBL; U30474; AAB40355.1; -.
HSSP; P05713; 3RAB.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005255; Smal_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                       -I- FUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULA TRAFFIC FROM ER TO GOLGI (BY SIMILARITY).
-I- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of a Phytophthora infestans
vesicle transport.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 52009;
MEDLINE-97128773; PubMed-8973313;
Chen Y., Roxby R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phytophthora infestans (Potato late blight fungus).
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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181:89-94(1996).
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(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
P-binding protein YPT1.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (PROBABLE).
GERANYL-GERANYL (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
MW: CD143BADB92B4C65 CRC64;
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Pred. No. 1.
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1.1e-46;
nes 27;
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                                                                                                                                             RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RR CSTRAIN-CV. Columbia;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Hheologis A., Ecker J.R., Palm C.J., Erderspiel N.R., Chin C.W.,

RA Hunter E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Pong B., Fujii C.Y.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Pong B., Fujii C.Y.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenettskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Jenz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nerman W.C., Osborne B.I.,

RA Malitscher J., Miranda M., Nguyen M., Neoney T., Rowley D.,

RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tallon L.J., Tambunga G., Torlumi M.J., Town C.D.,

RA Muterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

"Sequence and analysis of chromosome 1 of the plant Arabidopsis

"Talliana.",

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches 139
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GTF-binding;
NP_BIND
NP_BIND
NP_BIND
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARATH
SEQUENCE OF 64-258 FROM N.A.
STRAIN-Various strains; TISSUE-Leaf;
MEDLINE-92084144; PubMed-1748311;
Anai T., Hasegawa K., Watanabe Y., Uchimiya
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ras-related protein ARA-5.
ARA-5 OR ATIGO2130 OR T7123.6.
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Spermatophyta; Magnoliophyta;
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"Isolation and analysis of cDNAs
of arabidopsis thaliana.";
SEQUENCE FROM N.A. TISSUE=Coleoptile; MEDLINE=92115746;
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"Molecular cloning and structural analysis of genes from Zea may.
(L.) coding for members of the ras-related ypt gene family.";
Proc. Natl. Acad. Sci. U.S.A. 89.787-791(1992).
-1- EUNCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
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InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
InterPro; IPR005225; Small_GTP.
InterPro; IPR0071; ras; 1.
INTERPROPRIETS; PR00449; RASTRNSFRMNG.
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TISSUE SPECIFICITY: ITS EXPRESSION IS WEAK IN STEMS, HIGHER ROOTS, LEAVES AND COLEOPTILES, BUT HIGHEST IN FLOWERS.
PTM: THE PALMITIC ACID IS REQUIRED FOR MEMBRANE ATTACHMENT
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SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY
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MS; TIGR00231; small_GTP;
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Prenylation; Palmitate; Protein transport.
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Pred. No. 1.1e
1; Mismatches
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (PROBABLE).

PALMITATE (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).
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RESULT 14
YPT1_YEAST
ID YPT1_Y
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DT 21-JUI
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Best Local S
Matches 125
                                                                                             YPT1_YEAST
P01123;
21-JUL-1986
01-NOV-1995
15-JUN-2002
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                             21-JUL-1986 (Rel. 01, Created)
01-KOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
GTP-binding protein YPT1 (Protein YP2).
YPT1 OR YP2 OR YFL038C.
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SMART; S
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InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
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S; PR00449; RASTRNSFRMNG.
; SM00175; RAB; 1.
AMAS; TIGR00231; small_GTP
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25; Conservative
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FIGGO031: prenylation; palmitate; Protein trains, pro
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                                                                                                                                                                                                                           STANDARD;
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Pred. No. 2.
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InterPro; IPR003579; GTPase_Rab.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; par
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SEQUENCE FROM N.A.

MEDLINE-84093563; PubMed=6318115;

Gallwitz D., Donath C., Sander C.;

"A yeast gene encoding a protein ho
proto-oncogene product.";

Nature 306:704-707(1983).

[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WITAGENESIS OF EFFECTOR REGION.

WEDLINE-91184123; PubMed-2009858;

Becker J., Tan T.J., Trepte H.-H., Gallwitz D.;

Mutational analysis of the putative effector domain of the grap-binding typt protein in yeast suggests specific regulation by novel GAP activity.";

EMBO J. 10:785-792(1991).

1- FUNCTION: YPT1 IS ESSENTIAL FOR CELL VIABILITY. THE LOSS OF YP RESULTS IN CYTOSKELETAL AND MITOTIC LESIONS. YPT1 IS REQUIRED TRANSIT OF PROTEINS FROM THE ER THROUGH GOLGI COMPARTMENT.

1- PIM: THE PALMITIC ACID IS REQUIRED FOR MEMBRANE ATTACHMENT AND TRANSTANT THE PALMITIC ACID IS REQUIRED.
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(sb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS, AND POSSIBLE FUNCTION.
MEDLINE-88223356; PUDMEC-3286011;
Schmitt H.D. Puzicha M., Gallwitz D.;
"Study of a temperature-sensitive mutant of the ras-related YPT1 gene
product in yeast suggests a role in the regulation of intracellular
calclum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-88296440; PubMed-3042385; Molenaar C.M.T., Prange R., Gallwitz D.; Molenaar C.M.T., Prange R., Gallwitz D.; "A carboxyl-terminal cysteine residue is required for palmitic acid binding and biological activity of the ras-related yeast YPT1 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288C / AB972;

MEDLINE-95400292; PubMed-7670463;

Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,

Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyan

Yamazaki M., Tsahiro H., Eki T.;

"Analysis of the nucleotide sequence of chromosome VI from

Saccharomyces cerevisiae.";

Saccharomyces cerevisiae.";
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                                                                                                                                                                           EMBL; X00209; CAA25036.1; -.
EMBL; D50617; BAA09201.1; -.
PIR; A01374; TVBYQ2.
HSSP; P05713; 3RAB.
SGD; S0001856; YPT1.
SMART; SM00175; RAB; 1.
TIGRFAMs; TIGRO0231; small_GTP; 1.
GTP-binding; Lipoprotein; Protein transport; Golgi stack;
Endoplasmic reticulum; Prenylation; Palmitate.
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RESULT 15
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Best Local S
Matches 116
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LIPID
MUTAGEN
MUTAGEN
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CONFLICT
SEQUENCE
                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                   MEDLINE-94124041; PubMed-8294041;
Bush J.M. IV, Franck K., Daniel J.M., Spiegelman G.B., Weeks G., Cardelli J.A.;
"Cloning and characterization of five novel Dictyostelium discoideum rab-related genes.";
Gene 136:55-60(1993).
-- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                             RABA OR RABIA.

Dictyostelium discoideum (Slime mold).

Nycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                   RBIA_DICDI STANDARD; PRT; 167 AA. P34139; O1-FEB-1994 (Rel. 28, Created) O1-FEB 1994 (Rel. 28, Last sequence update) O1-OCT-1994 (Rel. 30, Last annotation update)
  DictyDb; DD05055; rabA.
InterPro; IPR003579; GT
InterPro; IPR001806; Ra
                                  EMBL; L21009; AAC37385.1; HSSP; P05713; 3RAB.
                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                   STRAIN-AX3
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             148
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l6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGP----G
                                                                                                                                                                                                                                                                                                                                                                                                                        TTQKKEDKGNVNLKGQSLTNTGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAGGAEKSNVKIQSTPVKQSGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKCDLKDKRVVEYDVAKEFADANKMPFLETSALDSTNVEDAFLTMARQIKESMSQQNLNE
IPR003579; GTPase_Rab.
IPR001806; Ras_trnsfrmng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I-----ESFNNVKQWLQEIDRYASENVNKLLVG
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                                                                                                                                                                                                                                                                                                            protein RablA.
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124
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GERANYL-GERANYL.
Y->F: NO CHANGE.
S->A: NO CHANGE.
T->S: NO CHANGE.
I->M: LETHAL.
V->E: NO CHANGE.
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Pred. No. 1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIP
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E -> Q (IN R
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F8C704F6BF2D227B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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(BY SIMILARITY).
(BY SIMILARITY).
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                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                           There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 206;
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Best Local S
Matches 111
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SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; sn
GTP-binding.
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DOMAIN
                                                                                                                                                                                         NP_BIND
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                    InterPro; IPR005225; Small_GTP
 121
                                                                                                                     al Similarity
111; Conserv
                    92
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                                                                            MNPEYDYLFKLLLIGDSGYGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
            NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMT 135
NKSDLVAKKVVDFNTAKAFADSLQIPFLETSAKQSTNVEQAFNT
                                      IWDTAGQERFRTITSSYYRGAHGIIVVYDVTDKLTFENVRQWLQEIDRFACENVNKLLVG
                                                                                                                                                                                                                       00175; RAB; 1.
TIGR00231; small_GTP; 1.
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67
124
45
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                                                                                                                               61.2%;
                                                                                                                                                             MW;
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                                                  Score 542; DB 1; Length 167; Pred. No. 2e-38; 0; Mismatches 11; Indels
                                                                                                                                                                   GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
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 164
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91

60

Search completed: June 18, 2003, 15:21:38 Job time: 23 secs

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                        Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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  SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
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886
1 MSSMNPEYDYLFKLLLIGDS......EKSNVKIQSTPVKQSGGGCC 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               671580 seqs, 206047115 residues
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	80	7	6	U	4	ω	N	_	No.	Result	
632	632.5	633	634.5	636.5	640	642	644	653.5	655.5	660	671	683	700	759.5	766.5	Score		
71.3	71.4	71.4	71.6	71.8	72.2	72.5	72.7	73.8	74.0	74.5	75.7	77.1	79.0	85.7	86.5	Match 1	Query	æ
202	· 203	202	202	203	202	202	202	201	201	205	202	205	141	201	201	Length DB		
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Ų,	024112 nicotiana p	Q9fpj4 arabidopsis	Q8w4s8 arabidopsis	Q08154 pisum sativ	Q9hdt5 trichoderma	. Q9seh3 arabidopsis	Q40203 lotus japon	Q9p8j7 aspergillus	Q9het3 aspergillus	Q9uaq6 caenorhabdi	O16143 bombyx mori		homo	Q9d1g1 mus musculu	Q9h0u4 homo sapien	Description		

443	38 40 40 10	34 35 37	30 32 33	25 27 28 29	.17 18 19 20 21 22 23
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Q40202 Q9HFM5 Q9BHN1 Q9BLF3	Q40201 Q25324 Q39274 Q9ZRE2	Q08152 Q9LGG3 Q43462 Q41339	Q8RU63 Q39861 Q96W97 Q9ZRH6	Q949E2 Q08155 Q940Z7 Q94153 Q08153 Q23594	Q40204 Q40569 Q40205 Q40205 Q9Y3T2 Q39845 Q3987P5 Q9M7P5 Q41338
Q40202 lotus japon Q9hfin kituyveromyc Q9bhn1 plasmodium Q9blf3 entamoeba h	Q40201 lotus japon Q25324 leishmania Q35324 brassica ca Q3274 brassica ca Q9zre2 arabidopsis	pisum sa oryza sa glycine	Q8ru63 oryza sativ Q39861 glycine max Q36w97 candida alb Q9zrh6 petunia hyb		040204 lotus japon 040569 nicotiana t 040569 nicotiana t 040205 lotus japon 039112 homo sapien 039845 glycine max 09m/p5 capsicum an 041381 lycopersico 041340 lycopersico

ALIGNMENTS

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kodo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kodo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Richi T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Richi R., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Ruchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Hyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Ra Hayashizaki Y.,
Pennettional and Allerath Massegawa Y., Kawaji H., Kohtsuki S.,
Ra Hayashizaki Y.,
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Best Local Sim
Matches 156;
   InterPro;
InterPro;
InterPro;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9D1G1;
Q9D1G1;
                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21085660; PubMed=11217851;
                                                            InterPro;
                                                                                                                                                                                                       TISSUE-KIDNEY;
                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1110011F09RIK
                                                                                                                                                                                                                                                                              'Functional annotation
                                                                                    unmitted (OCT-2001) to the li-similarity: TO RAS PROTEI BL; AK003609; BAB22888.1; BC016408; AAH16408.1; BP; P05711; 3RAB
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MGI:1923558; 1110011F09rik.

irPro; IPR003579; GTPase_Rab.

irPro; IPR001806; Ras_trnsfrmng.

irPro; IPR002078; Sig54_interact.

irPro; IPR005225; Small_GTP.
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| |: |:|| |||| :|||||
| G-ERPNLKIDSTPVKPAGGGCC 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=EMBRYO;
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77.2%;
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                                                                                                                                                                                                                                                                            of a full-length mouse
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17,
21,
                                                                                                                                                EMBL/GenBank/DDBJ databases EINS. BELONGS TO THE RAB SUB
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Last annotation updat
N cDNA 1110011F09 gene
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Pred. No. 4.1e
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ESFNNVKQWLQEIDRYASENVNKLLVG
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7;
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9 gene).
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Best Local S
Matches 154
                                                                                       Matches
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CDNA FLJ31365 fis, Clone NROW'
protein RAB-la
                                                                                                                                                                                                                   "NEDO human cDNA sequencing project. Submitted (CCT-2001) to the EMBL/Gen EMBL; AK055927; BAB71048 l; InterPro; IPR001806; Ras_trnsfrmng. InterPro; IPR002078; Sig54_Interact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRPAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1;
                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                             Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S
Fukurumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Is
Kawai-Ho Y., Saito K., Nishikawa T., Kimura K., Yamashita
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96N61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTP-binding; Lipoprotein. SEQUENCE 201 AA; 22187 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96N61
                                                                                                                                                       Pfam; PF00071;
PROSITE; PS006
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                                                                                                  Similarity
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           KLQIESFNNVKQWLQEIDRYASENVNKLLVGNKCDLTTKKVVDYTTAKEFADSLGIPFLE
                                                       MSSMNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTI
                                                                                                                                                      PS00675;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKCDLITKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG
                                          MSSMNPEYDYLFKLLLIGDSGVGKSCLLLRFA---
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                                                                                                                                   141
                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
ESFNNVKQWLQEIDRYASENVNKLLVGNKCDLTTKKVVDYTTAKEFADSLGIPFLE
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                                                                                                                                                                   ras;
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                                                                                                                                                     SIGMA54_INTERACT_1;
                                                                                                                                   15330 MW;
                                                                                                 79.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                 19, Last sequence update)
20, Last annotation update)
NB9N41000135, highly similar to
                                                                                                                                                                                                            project.";
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 759.5;
Pred. No. 1.5e
7; Mismatches
                                                                                      Score 700; DB 4;
Pred. No. 5.8e-49;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                 620F588CA34B3A77 CRC64;
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                                                                                                                                                       UNKNOWN_1.
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8;
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                                                                                                            Length 141;
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AC 0183

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RA CHEIL
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RA Addams N.D., Celniker S.E., Hichards S., Ashburner M., Henderson S.N.,
RA George R.A., Levais S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Maldwin D.,
RA Beeson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bertis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
RA Lasko P., Cawley L., McDavies J., Ranger K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Merkulow G., Milshina N.V., Mobarry C., McDien J.A., Noshrefi A.,
RA Lasko P., Leith R., Kalpen G., Leith R.,
RA Merkulo
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endoptera; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          018332
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-OREGON R; TISSUE-HEAD;
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01-JUN-2002
                                                                                                                                                                    MEDLINE-97228579; PubMed-9074639;
Satoh A.K., Tokunaga F., Ozaki K.;
"Rab proteins of Drosophila melanogaster: novel members of the Rab-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
(TrEMBLrel. 05, (TrEMBLrel. 05, (TrEMBLrel. 21,
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Last annotation update)
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                                                                                                                           GTP-binding; Lt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bombyx mori (Silk moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoldea; Bombycldae; Bombyx.
NCBI_TaxID-7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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SEQUENCE 205 AA; 22762 MW; 9CE2691205FAE343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGREAMS; TIGR00231; Small_GTP; 1.
PROSITE; P800675; SIGMA54_INTERACT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003579; GTPase_Rab.
InterPro; IPR0031806; Ras_trnsfrmg.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR002525; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                     TIGREAMS; TIGRO0231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1
                                                                                                                                                                                                                                                      PRINTS; PRO0449; RAS; SMART; SM00175; RAB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Small GTP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P05713; 3RAB.
FlyBase; FBgn0016700; Rabl.
                                                                                                                                                                                                                                                                                                                                             HSSP; P05713; 3RAB.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; S1954_interact.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jno T., Nakajima A., Ueno M., Alzono Y.;
"Isolation of cDNA encoding small GTP-binding protein from Bombyx
                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF013572; AAB67169.1; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                   PF00071; ras;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 LVGNKCDLITKKVVDXTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KLQIWDTAGQERFRTITSSYYRGAHGIIVVYDCTDQESFNNVKQWLEEIERYACENVNKL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSSMNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSSVNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SATD-NASKVKIDQGRPVENTKSGCC 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGGAEKSNVKI-QSTPVKQSGGGCC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                              Lipoprotein
02 AA; 2236
                                                                                                                                                                                                                                                                                      RASTRNSFRMNG.
                                                                                                                              22364 MW; 0338E895D63CDFE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.1%; Score 683; DB 5; Length 205; 69.4%; Pred. No. 2.2e-47;
75.7%; Score 671; DB 5 66.5%; Pred. No. 2e-46; tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches
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Last annotation update)
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                                                                 DB 5; Length 202;
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Matches 135;

Conservative

16; Indels

34:

Gaps

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RESULT 6
Q9UAO6
AC Q9UAO6
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                                                                                               Query Match
Best Local S
Matches 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 22.5 kDa protein.
C39F7.4.
                                                                                                                                                                                       PRINTS; PRO0449; RASTRNSFRANG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; Small_GTP; 1.
TRIGROSSITE; PROS675; SIGMA54_INTERACT_1; UNKNOWN_1.
GTP-binding; Hypothetical protein; Lipoprotein.
SEQUENCE 205 AA; 22545 MW; 5221920FD05842D3 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scheet P., Maggi L., Dubbelde C., "The sequence of C. elegans cosm: Submitted (OCT-1998) to the EMBL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UAQ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases - SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBLEMBL, AF101310; AAC69218.1; -. HSSP; P01112; 1PLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                       Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nemato Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science
                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology. The C
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. e. investigating biology. The C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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                                                                                                                                                                                                                                                                                                                                     PF00071; ras;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
                                                                                                 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAEKSNVKI-QSTPVKQSGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAPAGHVKIDQGQPIDTGKSSCC
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                                                                                                                                                                                                                                                                                                                                                        IPRO03579; GTPase_Rab.
IPRO01806; Ras_trnsfrmng.
IPRO02078; S1g54_interact.
IPRO05225; Small_GTP.
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nematoda;
                                                                                                                       74.5%;
66.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pda; Chromadorea; Rhabditida; Rhabditoidea;
Caenorhabditis
                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cosmid C39F7.";
EMBL/GenBank/DDBJ
                                                                                            Score 660; DB 5;
Pred. No. 1.5e-45;
6; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans: a platform for sequencing Consortium.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                 18;
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                                                                                                                                                                                              CRC64;
                                                                                                                                           Length
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFAMILY
                                                                                                                                             205;
                                                                                               36;
                                                                                            Gaps
    60
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification and characterisation of a family of secretion related small GTPase encoding genes from the filamentous fungus Aspergillus niger: a putative SEC4 homologue is not essential for growth."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY. EMBL, AJZ78659; CA17833.1; --
EMBL, AJZ78659; CA17833.1; --
HSSP; P01112; 1PLJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGREAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002778; Sig54_interact.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-N402;
Punt P.J., Selboth B., We
Punt P.J., Selboth B., We
Konetschny C., Ram A.F.,
Van Den Hondel C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiom
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9HET3;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP-binding;
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  178
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                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                       Similarity
                           GAEKSNVKIQSTPVKQSG--GGCC
                                                                                                                                                                                                                                                          MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        001 (TremBLrel. 10001 (TremBLrel. 10002 (TremBLrel. 2002 (TremBLrel. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGA - - PGVRITGSQPVQDKKSGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLQI-----ESFNNVKQWLQEIDRYASENVNKL
VNNKPTVQVGQGQGVQSGSAGGCC
                                                                                 NKSDMEDKKVVEYTVAKEFADSLGIPFLETSAKNASNVEQAFLIMARQIKERMG---TAT
                                                                                                      NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG
                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipoprotein.
01 AA; 22303 MW;
                                                                                                                                                                                                                                                                                                                                                                    74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 16, Created)
. 16, Last sequence update)
l. 21, Last annotation update
ase (SrgB).
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                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                           Score 655.5; I
Pred. No. 3.4e:
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                      8DC1A5B0BEBDF378 CRC64;
  20
                                        173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       van Zeijl C.M.,
Kubicek C.P.,
                                                                                                                                                                                               ----ESFNNVKQWLQEIDRYASENVNKLLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
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                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
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                                                                                                                                                                                                                                                                                                                                                  18;
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                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                           201;
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                                                                                                                                                                                                                                                                                                                                              Gaps
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Best Loc
Matches
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InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR005225; Small_GTP.
Pfam; Pr00071; ras; 1.
PRINTS; PR00449; RASTRNSFRNNG.
PRINTS; PR00449; RASTRNSFRNNG.
SMART; SW00175; RAB; 1.
SMART; SW00175; RAB; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
SEQUENCE 201 AA; 22335 MW; 9D710FB1AEBDE279 CRC.
                                                                     Q40203
Q40203;
Q1-0VV-1996
Q1-NOV-1996
Q1-JUN-2002
RABIC.
RABIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9P8J7;
Q9P8J7;
01-OCT-2000
01-OCT-2000
01-JUN-2002
          Lotus japonicus.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids I; Fabales; Fabaceae; Papillonoldeae; Loteae; Lotus.

NCBI_TaxID=34305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL: AR244545; AAF63333.1; -.
HSSP; P01112; 1PLJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The secretory genes yptl/yptA and nsf1/nsfA from the filamentous fungi Trichoderma reesei and Aspergillus niger: evidence for globs transcriptional regulation of the secretory pathway in Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus awamori.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID-105351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penttila M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Saloheimo M., Wang H., Valkonen M., Vasara T.,
                                                                                                                                                                         ø
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 67.:
es 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Match
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                                                                                                                                                                                                                          GAEKSNVKIQSTPVKQSG--GGCC 173
                                                                                                                                                                                                                                                                                                                          NKSDMEDKKVVEYTVAKEFADSLGIPFLETSAKNASNVEQAFLTMARQIKERMG---TAT
                                                                                                                                                                                                                                                                         NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG
                                                                                                                                                                                                                                                                                                                                                          MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTMKLQ
                                                                                                                                                                                                            VNNKPTVQVGQGQGVQSGSAGGCC
                                                                                                                                                                                                                                                                                                          IWDTAGQERFRTITSSYYRGAHGICVVYDVTDMDSFNNVKQWLQEIDRYATEGVNKLLVG
                                                                                              G (TrEMBLrel.
G (TrEMBLrel.
G (TrEMBLrel.
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                                                                                                                                                PRELIMINARY;
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15,
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                                                                                              Created)
Last sequence update)
Last annotation updat
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                           Score 653.5; DB 3; Length 201;
Pred. No. 5e-45;
2; Mismatches 18; Indels 37
                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9D710FB1AEBDE279 CRC64;
                                                                                                                                                                                                            201
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                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                            37;
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Best Local S
Matches 133
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InterPro; IPR003579; GTPase_Rab.
InterPro; IPR003078; S1954_Interact.
InterPro; IPR003025; Small_GTP.
InterPro; IPR005025; Small_GTP.
InterPro; IPR005025; Small_GTP.
INTERPARS; TIGR0075; RAB; 1.
ITGRPAMS; TIGR00731; Small_GTP; 1.
ITGR00715; SMALL_GTP; 1.
ITGRPAMS; TIGR00731; SMALL_GTP; 1.
ITGR00715; SMALL_GTP; 1.
ITGR0071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9SEH3 PRELIMINARY; PRT; 202 AA.
Q9SEH3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
RAS-related small GPP-binding protein (RAS-related;
protein RABIC) (AT4G17530/DL4800C).
RABIC OR AT4G17530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-ROOT NODULES;
MEDLINE-97231679; Pubbed-9076991;
MEDLINE-97231679; Pubbed-9076991;
Borg S., Brandstrup B., Jensen T.J., Poulsen C.;
Tidentification of new protein species among 33 different
"Identification of new protein species among 33 paponicus, an
binding proteins encoded by cDNAs from Lotos japonicus, an
of corresponding mRNAs in developing root nodules.";
Plant J. 11:237-250(1997).
SEQUENCE FROM N.A. Cheuk R., Chen H.,
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA; TISSUE-EPIDERMAL;
BISCHOFf F., Godde M., Palme J.;
BISCHOFF F., Godde M. Palme J.;
"Atkable involved in ER-Golgi traffic
Arabidopsis.";
Submitted (FEB-1999) to the EMBL/GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                    SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: TO RAS PROEMBL; Z73932; CAA98160.1; HSSP; P05713; 3RAB.
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    Kim C.J.,
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                                                                                                                                                                                                                                                                                                        ., Palme J.;
ER-Golgi traffic in
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                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
        Koesema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91633EBFAD07662F CRC64;
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2.9e-44;
                                                                                                                                                                                                                                                                                                            meristematic cells
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    Meyers M.C., Banh
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RESULT 11
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Best Local S
Matches 133
Submitted (MAR-2000)
-i- SIMILARITY: TO RA
EMBL; AJ277108; CAC17
                                                                                 STRAIN-RUTC-30;
Saloheimo M.L.A., Wanng
Riikonen M., Pakula T.,
                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
Small GTP-binding protein Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                 for g
                                                                        "The
                                                                                                                                               Trichoderma reesei (Hypocrea jecorina).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreales; Hypocreaceae; Hypocrea.
MCBI_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Liam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Kawai J., Lam B., Lee J.M., Elm, J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                Q9HDT5;
                                                                                                                                                                                                                                                                           Q9HDT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP-binding; Lipoprotein.
VARIANT 70 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY
L; AF127134; AAF22133.1; -.
L; AL161546; CAB78756.1; -.
L; AV052204; AAK97675.1; -.
P; P05713; 3RAB.
                                               konen M., Pakula T., Ward M., Penttilae M.; e secretory genes yptl/yptA and nsfl/nsfA from the filamer gi Trichoderma reesei and Aspergillus niger var. awamori: global transcriptional regulation of the secretory pathwa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO0449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                       GSKPPTVQIRGQPVNQQ-SGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                     MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
                                                                                                                                                                                                                                                                                                                                                                GAEKSNVKIQSTPVKQSGGGCC
                                                                                                                                                                                                                                                                                                                                                                                      NKCDLTSQKVVSTETAKAFADELGIPFLETSAKNATNVEEAFMAMTAAIKTRMA-SQPAG
                                                                                                                                                                                                                                                                                                                                                                                                     NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNAINVEQSFMTMAAEIKKRMGPGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003579; GTPase_Rab.
IPR001806; Ras_trnsfrmng.
IPR002078; Sig54_Interact.
IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 AA;
                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
 TO RAS PR
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22318 MW;
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                        to the EMBL/GenBank/DDBJ
  PROTEINS.
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                                                                                                 Valkonen M.,
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                                                                                                                                                                                                                                                   Created)
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Pred. No.
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954FA24C3110FC12
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            BELONGS
                                                                                                                                                                                                                                                                           202
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4.2e-44;
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           THE RAB
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                        databases
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           SUBFAMILY
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Query Match
Best Local S
Matches 131
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Best Local Sin
Matches 134;
                                                                                             InterPro; IPR001806; Ras trasfrmg.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR005225; Small_GTP.
Pfam; PR00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; Small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UN
GTP-binding; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Creation of the Control of 
                                                                                                                                                                                                                               InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                       "Isolation and characterization of cDNAs binding protein from Pisum sativum."; plant Cell Physiol. 34:447-455(1993).
-!- SIMILARITY: TO RAS PROTEINS. BELONGS EMBL; D12549; BAA02117.1; -.

HSSP; P05713; 3RAB.
InterPro; IPR003579; GTPase_Rab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO0231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
SEQUENCE 202 AA; 22421 MW; A660E10E2AB1B2E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94290824; PubMed=8019783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q08154;
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InterPro; IPR002078;
InterPro; IPR005225;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3888;
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il Similarity
131; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Y., Murai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003579;
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                                                                                  A,
                                                                                                                                                                                                                                                                                                                                                                                                                                           N., Matsuno R.,
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Sig54_interact.
Small_GTP.
                                                                                  22463 MW;
                   71.8%;
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Last sequence update)
Last annotation updat
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Pred. No. 6.1e
13; Mismatches
                   Score 636.5;
Pred. No. 1.
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                                                                                  6F2E1007A31EF3F4 CRC64;
  Mismatches
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                                                                                                                           UNKNOWN_1
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                                         DB 10;
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                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 131
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01-MAR-2002 (TREMBLrel. 20, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
AT4917530/d14800c.
AT4917530/d14800c.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID-3702;
                                                                                                                                                                                                                                                                                            "Arabidopsis ORF clones.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY060495; AAL31108.1; -.
InterPro; IPR003579; GFPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; S1g54_Interact.
Pfam; PF00071; ras; 1.
PRINTS; PR000449; RASSTRNSFRANG.
SMART; SM00175; RAB; 1.
PROSSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
SEQUENCE 202 AA; 22286 MM; 954FA12C3110FC12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,

Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,

Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,

Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith R.D.,

Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,

Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,

Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou

Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,

Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8W4S8
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GAEKSNVKIQSTPVKQSGG
|:: |:|: || | |
| GSKPPTVQIRGQPVNQQSG
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NARPPTYQIRGQPYGQK-GGCC 201
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                                                                                                                                   IWDTAGQERFRTITSSYYRGAHGIIIVYDVTDEESFNNVKQWLSEIDRYASDNVNKLLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKCDLTSQKVVSTETAKAFADELGIPFLETSAKNATNVEEAFMAMTAAIKTRMA-SQPAG
                                                                             NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG
                                                                                                                                                                           MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDSYLDSYISTIGVDFKIRTVEQDGKTIKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I-----ESFNNVKQWLQEIDRYASENVNKLLVG
                                                                                                                    IWDTAGQERFRTITSSYYRGAHGIIVTYDVTDLESFNNVKQWLNEIDRYASENVNKLLVG
                                                                                                                                                                                                                                    ilarity 65.8
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                    71.6%;
                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                  Score 634.5; DB 10; Length Pred. No. 1.7e-43; Indels 24; Indels
   198
                               170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
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                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                      Gaps
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Query Match
Best Local Sin
Matches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARABIGOSSIS Full Length CDNA Clones.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

SUBMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMI

EMBL; AF324990; AAG40342.1; -.

EMBL; AF034991; AAG40342.1; -.

EMBL; AF080753; AAL65999.1; -.

R EMBL; AF080753; AAL65999.1; -.

R InterPro; IPR003379; GTPase_Rab.

InterPro; IPR003379; GTPase_Rab.

InterPro; IPR003078; Sig54_Interact.

InterPro; IPR002078; Sig54_Interact.

R InterPro; IPR002078; Sig54_Interact.

R Pfam; PF00071; ras; L. ENCERNIERUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSPPJ4 PRELIMINARY; PRT; 202 AA.

OSPFJ4;

O1-MAR-2001 (TrEMBLrel. 16, Created)

O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)

O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)

O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)

AT5947200 (Putative ras-related small GTP-binding protein).

AT5947200/MOL5 5 OR AT5947200.

AT5947200/MOL5 5 OR AT5947200.

AT5947200/MOL5 5 OR AT5947200.

AT5947200/MOL5 5 OR AT5947200.

AT5947200/MOL5 1 Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidellar annotation in the sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0449; RASTRINSFRANG.
SMART; SM00175; RAB; 1.
TIGREAMS; TIGRO0231; Small_GTP; 1.
PROSITE; PS00675; SIGMAS4_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
SEQUENCE 202 AA; 22313 MW; D0129A296C3EFDFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser I Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shinn P., Chao Q., Brooks S., Chen H., Cheuk R., Johnson-Hopson C., Khan S., Kim C.J., Banh J., Bowser L., Chung M.K., Goldsmith A.D., Jones T., Karlin -Neumann G., Lam B., Lee J.M., Lin J., Liu S. X., Miranda M., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Southwick A., Toriumi M., Yamada K., Yu G., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Yamada K., Liu S.X.,
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Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Arabidopsis cDNA clones.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                121
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                                                                                                                                                                                                                                                                                                 Similarity
                              GAEKSNVKIQSTPVKQSGGGCC
                                                                                                                        NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG
                                                                                                                                                                                              GAKPPTVQIRGQPVNQQ-SGCC
                                                                                                   NKNDLTSQKVVSTETAKAFADELGIPFLETSAKNATNVEEAFMAMTAAIKTRMA-SQPAG
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        71.4%; Score 633; DI 65.8%; Pred. No. 2.20 tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D0129A296C3EFDFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 2.2e-43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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., Jones T.,
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RESULT 15
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Search completed: June 18, 2003, 15:23:06
Job time: 82 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001230; F
InterPro; IPR001806; R
InterPro; IPR002078; S
InterPro; IPR005225; S
                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0449; RASTRNSFRANG.
SMART; SM00175; RAB; 1.
TIGREAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
PROSITE; PS00675; SIGMA54_INVERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
SEQUENCE 203 AA; 22516 MW; 13799234FF719DE7 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       024112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Small GTP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Borisjuk N., Sitailo L., Kaydamov C., Senger S., Tewes A.,
Manteuffel R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y08425; CAA69701.1; HSSP; P01112; 1PLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003579; GTPase_Rab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4092;
                                                    152 GAEKSNVKIQSTPVKQSGGGCC 173
| |:|: || | || |
181 NARPPTVQIRGQPVNQK-SGCC 201
                                                                                                           121 NKCDLTAQKVVSTETAQAFADEIGIPFMETSAKNATNVEQAFMAMAASIKNRMASQPASN 180
                                                                                                                                       92
                                                                                                                                                                  61
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                                                                                                                                                                                                                   NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Prenyl_site.
; Ras_trnsfrmng.
; Sig54_interact.
; Small_GTP.
                                                                                                                                                                                                                                                                                                                                 22516 MW; 13799234FF719DE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 AA
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                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                               120
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Title: Perfect score: Sequence:

US-09-820-003B-2 886

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Run

OM protein

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          June 18, 2003, 15:21:20 ; Search time 27 Seconds (without alignments) 188.525 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSSMNPEYDYLFKLLLIGDS.....EKSNVKIQSTPVKQSGGGCC
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Copyright (c) 1993 - 2003 Compugen Ltd
                        US-08-531-525-13
US-08-916-901-3
US-08-916-901-3
US-09-154-602-3
US-09-154-602-8
US-09-154-602-8
US-08-918-2708-14
US-08-718-2708-10
US-08-718-2708-35
US-08-718-2708-35
US-08-718-2708-25
US-08-718-2708-21
US-08-718-2708-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262574
Sequence 13, Appli Sequence 3, Appli Sequence 3, Appli Sequence 8, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 15, Appli Sequence 35, Appli Sequence 35, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 27, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 31, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173
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Sequence 13, Application US/08531525

Patent No. 5840683

GENERAL INFORMATION:
APPLICANT: Hlawka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: No. 58406831e, John F.
APPLICANT: Kende, Andrew S.
ITILE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: of P21 Ras

NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
                                                                                                COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PolyMS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 37-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEPAX: (303) 499-8080
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: TOPOLOGY: linear
MOLECULE TYPE: Protein
MOLECULE TYPE: Protein
MYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Discopyge ommata
                                                                              US-08-531-525-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-08-531-525-13
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80303
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   91.8%;
81.2%;
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US-08-718-270A-16
US-08-718-270A-52
US-08-718-270A-52
US-08-718-270A-13
US-09-198-184-3
US-09-198-184-3
US-08-718-270A-11
US-08-718-270A-11
US-08-718-270A-36
US-08-718-270A-36
US-08-718-270A-15
US-08-718-270A-15
US-08-718-270A-26
US-08-718-270A-26
US-08-718-270A-26
US-08-718-270A-26
US-08-718-270A-26
Score 813.5; DB 2;
Pred. No. 2.3e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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                           Length
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Sequence 52, Appl
Sequence 52, Appl
Sequence 53, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
                        201;
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Result No.

813.5 813.5 766.5 766.5 760.5 702.5 702.5 439 424 418

417.5 417.5 417.5 390 390 366 366 334 334 330.5 330.5 330.5

991.8 866.5

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64

Matches

164;

201;

33;

Gaps

120 91 60

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TELEFAX: (303) 499-80 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                   MOLECULE TYPE: pr
                                                                                                                                                                                                                                                                  FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                         ORIGINAL SOURCE:
                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 21-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 20-SE
                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                     REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LE OF INVENTION: Peptidomimetics Inhib
LE OF INVENTION: the Oncogenic Action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13, 5510478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boulder
                                                                                                                                                                                                                                                 Ferber, Donna M.
                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAEKSNVKIQSTPVKQSGGGCC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNPEYDYLFKLLLIGDSGYGKSCLLLRFADDTYTESYISTIGYDFKIRTIELDGKTIKLQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSEKSNVNIQSTPVKSSGGGCC 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLQEIDRYASENVNKLLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hlavka, Joseph J.
Pincus, Matthew R.
No. 59104781e, John F.
Abajian, Henry B.
Kende, Andrew S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08718270A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Greenlee, Winner and Sullivan, P.C 5370 Manhattan Circle, Suite 201
                                                                                                                    201 amino acids
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      Discopyge ommata
                                                                       linear
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                      (303)
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                                                    protein
                                                                                    single
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                  Query Match
Best Local Similarity
     Matches
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                                                                                                                                                                                                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 201 amino acid
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                              FILING DATE: Filed Herewith PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 9
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APPLICANT: Shah, F
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                     MEDILL LIBRARY: LIBRARY: 2514506
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OPERATING SYSTEM:
                                                                                                                                                                     TYPE:
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                                                                                                                                  TOPOLOGY:
                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                               NAME: Billings, Luc
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                  amino acid
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                  86.5%;
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81.2%;
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Score 766.5; DB 2;
Pred. No. 7.3e-82;
6; Mismatches 7;
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Pred. No. 2.3
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COUNTRY:

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RESULT 2 US-08-718-270A-13

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121 92 61

33;

Gaps

2

TOPOLOGY:

ORGANISM:

LENGTH:

TELEPHONE:

Query Match 86.5%; Score 766.5; DB 4; Length 201; Best Local Similarity 77.2%; Pred. No. 7.3e-82; Matches 156; Conservative 6; Mismatches 7; Indels 33; Gaps 2; Qy 4 MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ 63	; INFEDIATE SOURCE: ; INFEDIATE SOURCE: ; LIBRARY: LIVRTUTO4 ; CLONE: 2514506 US-09-154-602-3	ES 20 A	; FILING DATE: ; ATTORNEY/AGENT INFORMATION: ; NAME: Billings, Lucy J. ; NAME: Billings, Lucy J. ; REGISTRATION NUMBER: 36,749 ; REFERENCE/DOCKET NUMBER: PP-0367 US : TELEFORMYNINGATION INFORMATION:	APPLICATION NUMBER: US/09/154,602 FILING DATE: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/916,901	# \$ 2 2 2 5 F	CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pharmaceuticals, Inc. STREET: 3174 Forter Dr. CITY: Palo Alto STATE: CA COUNTY: USA COUNTY: USA ZIP: 94304	Areto C	Qy 152 GAEKSNVKIQSTPVKQSGGGCC 173 : :	Db 1 MNPEYDYLFKLLLIGDSGYGKSCLLLRPADDTYTESYISTIGVDFKIRTIELDGRTIKLQ 60 Qy 64 IESFNIVKQMLQEIDRYASENVIKLLVG 91
Qy 4 MNPEZDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDEKIRTIELDGKTIKLQ 63	Ouery Match 85.8%; Score 760.5; DB 2; Length 201; Best Local Similarity 76.2%; Pred. No. 3.7e-81; Matches 154; Conservative 7; Mismatches 8; Indels 33; Gaps 2;	TYPE: amino acid STRANDENESS: single TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: GenBank CLONE: 57006 US-08-916-901-8	NICATI NE: 4 : 415 FOR S CHARAC	ATTORNEY AGENT INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0367 US	LICATION DATA: LICATION DATA: ON NUMBER: U\$/08/916,901 TE: Filed Herewith CATION DATA: CATION DATA:	STATE: CA COUNTRY: USA ZIP: 94304 ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible COMPUTER: OSSIEM: DOS OPERATING SYSTEM: DOS OPERATERS: FRASTER FOR WINDOWS VARSION 2 0	GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L. APPLICANT: La1, Preet1 APPLICANT: Corley, Neil C. APPLICANT: Shab, Purvi TITLE OF INVENTION: RAB PROTEINS NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto	RESULT 5 US-08-916-901-8 ; Sequence 8, Application US/08916901 ; Patent No. 5892012	Db 61 IWDTAGGERFRITTSSYYRGAHGIIVVIDVIDQESYANVKQWLQEIDRYASENVNKLLVG 120 92 NKCDLTTKKVVDYTTAKEFADSLGIFFLETSAKNATNVEQSFMTMAAEIKKRWGPGATAG 151

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US-09-154-602-8
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TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
TYPE: amino acid
                                                                                                                                                                                                                          Query Match 85.8%;
Best Local Similarity 76.2%;
Matches 154; Conservative
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
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REGISTRATION NUMBER: 36,749
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181 G-ERPNLKIDSTPVKSASGGCC 201
                          152 GAEKSNVKIQSTPVKQSGGGCC 173
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3174 Porter Dr.
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Pred. No. 3.7e-81;
7; Mismatches 8
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Best Local S
Matches 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ferber; Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 37-9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: pi
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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ZIP: 80303
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
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                                 149
 179
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                                                                                                                            61 KLQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLQEIDRYASENVNKL 120
                                                                                                                                                               61 KLQI----
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                                                                                                                                                                                                              1 MSSMNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTI
                                                                                                                                                                                                                                                                          Similarity
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                                                                                LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGA 148
 TASDS-KPSVKINSSTPSANKGGCC
                              TAGGAEKSNVKIQSTPVKQSGGGCC 173
                                                               LVGNKSDLTTKK-VDFTTAKEYADQLGIPFLETSAKNATNVEQAFMTMAAEIKNRMGP-I 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 amino acids
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5370 Manhattan Circle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kende, Andrew S
                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 58406831e, John F. Abajian, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hlavka,
                                                                                                                                                                                                                                                                                                                                      Lymnea stagnalis
                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                        79.3%; Score 702.5; 72.2%; Pred. No. 2.36 tive 9; Mismatches
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Suite
202
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                                                                                                                                              -ESFNNVKQWLQEIDRYASENVNKL
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RESULT 8 US-08-718-270A-14

Sequence 14, Application US/08718270A

atent No. 5910478

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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Lymnea stagnalis
US-08-718-270A-14
RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (303) 499-801
TELEPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/531,525
FILING DATE: 21-SEP-1995
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
COMPUTER: PRINT PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/004,091 FILING DATE: 21-SEP-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Peptidomimetics Inhibiting TITLE OF INVENTION: the Oncogenic action of P21 Ras NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 202 amino
TYPE: amino acid
STRANDEDNESS: sir
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CITY: Boulder
STATE: Colorado
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                                                            179
                                                                                           149 TAGGAEKSNVKIQSTPVKQSGGGCC 173
                                                                                                                                     121 LYGNKSDLTTKK-YDFTTAKEYADQLGIPFLETSAKNATNVEQAFMTMAAEIKNRMGP-I 178
                                                                                                                                                            89 LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGA 148
                                                                                                                                                                                                               61 KLQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLQEIDRYASENVNKL
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                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                          TASDS-KPSVKINSSTPSANKGGCC 202
                                                                                                                                                                                                                                                                                               MSTMNPDYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTI
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Pincus, Matthew R.
No. 59104781e, John F.
Abajian, Henry B.
Rende, Andrew S.
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RESULT 10
US-08-718-270A-10
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fezber, Donna M.
REGISTRATION UNMER: 33,878
REFERENCE/DOCKET NUMBER: 37-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8000
TELEPAY
Sequence 10, Application US/08718270A Patent No. 5910478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 49.5%; Score 439; DB 2; Length 215; Best Local Similarity 45.4%; Pred. No. 2e-43; Matches 93; Conservative 28; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/531,525
FILING DATE: 21-SEP-1995
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APPLICANT: Pincus, Matthew R.
APPLICANT: No. 58406831e, John
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action TITLE OF INVENTION: of P21 Ras
                                                                                                                                                                                155 KSNVKIQSTPVKQSGG-----GCC 173
                                                                                                                                                                                                                      131 MDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVEEVFFSIGRDIKQRLSD--TDSRAE 188
                                                                                                                                      189 PATIKISQTDQAAGAGQATQKSACC 213
                                                                                                                                                                                                                                                                                                                                                                            11 DYDYLIKLLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIWD 70
                                                                                                                                                                                                                                                         96 L-TTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAGGAE 154
                                                                                                                                                                                                                                                                                                 71 TAGQERRTITTAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQHASDNVNKILVGNKAD 130
                                                                                                                                                                                                                                                                                                                                       Boulder
Colorado
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5370 Manhattan Circle, Suite 201
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                RESULT 11
US-08-531-525-35
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Sequence
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ORIGINAL SOURCE:
ORGANISM: Ara
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APPLICATION NUMBER: US 08/531,525
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CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ferber, Donna M. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 20-SE
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                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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 35, Application US/08531525
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                                                                                                                                                               L-TTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAGGAE 154
                                                                                                                                                                                                   TAGQERRTITTAYYRGAMGILLYYDYTDESSFNNIRNWIRNIEQHASDNYNKILYGNKAD 130
                                                                                                                                                                                                                                                                                   EYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQI--
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                                                                           PATIKISQTDQAAGAGQATQKSACC 213
                                                                                                        KSNVKIQSTPVKQSGG-----GCC 173
                                                                                                                                                                                                                                                                  DYDYLIKLLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIWD 70
                                                                                                                                       MDESKRAVPTAKGQALADEYGIKFFETSAKTNLNVEEVFFSIGRDIKQRLSD--TDSRAE 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 amino acids
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Pincus, Matthew R.
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N: 514
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45.4%; Pred. No. 2e-43;
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Sequence 35, Patent No. 5

5, Application US/08718270A 5910478

GENERAL INFORMATION:

APPLICANT:

Hlavka, , Pincus, ,

Matthew R.

Joseph J.

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US-08-718-270A-35
               RESULT 12
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US-08-531-525-35
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTURNET, AND A M.

NAME: Ferber, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER: 37-9

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                  124 EKRQVSKERGEKLAIDYGIKFLETSAKSSINVEEAFITLARDIMTKLNKKNNENSLQEAV 183
                                                                                      158 VKIQSTPVKQS 168
                                                          184 DKLKSPPKKPS 194
                                                                                                                                                   98
                                                                                                                                                                                64 AGQERFRTITAYYRGAMGIMKVDITNEKSFDNIKNWIRNIEEHASSDVERMILGNKCDMN
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                                                                                                                                                                                                                                        8 YDYLFKLLLIGDSGYGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQI---
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                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                 TKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAGGAEKSN 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 amino acids
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                                                                                                                                                                                                                                                                                                      Conservative
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Kende, Andrew S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 58406831e, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pincus, Matthew R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hlavka,
                                                                                                                                                                                                                                                                                                                                                                             Discopyge ommata
                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                  47.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides Inhibiting the Oncogenic Action of P21 Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/531,525
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                                                                                                                                                                                                                                                                                                                 Score 424; DB 2;
Pred. No. 1.1e-41;
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                                                                                                                                                                                                            ----ESFNNVKOWLQEIDRYASENVNKLLVGNKCDLT 97
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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Discopyge ommata
US-08-718-270A-35
                                                              US-08-824-873-4
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                    Sequence 4, Application US/08824873 Patent No. 5843717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/718,270A
FILING DATE: 20-SEP-1996
CLASSIFICATION UNMER: US 08/531,525
FILING DATE: 21-SEP-1995
PRIOR APPLICATION MUMBER: US 08/531,525
FILING DATE: 21-SEP-1995
PRIOR APPLICATION NUMBER: US 08/531,525
FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
NUMBER: FESTACT DOGGA WINDER: US NUMBER: US 60/004,091
FILING DATE: 21-SEP-1995
ATTORNEY/AGENT INFORMATION:
  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
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APPLICANT: Abajian, Henry B.

APPLICANT: Kende, Andrew S.

PITTLE OF INVENTION: Peptidominetics Inhibiting

FITTLE OF INVENTION: TO Oncogenic Action of P21 Ras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78
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                                                                                                                                                    184 DKLKSPPKKPS 194
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                                                                                                                                                                                                                                                                                                                       64 AGQERERTITAYYRGAMGIMKVDITNEKSFDNIKNWIRNIEEHASSDVERMILGNKCDMN 123
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US-09-198-184-4
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Best Local S
Matches 84
ADDRESSEE:
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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 234746
US-08-824-873-4
                                                     Sequence 4, Application US/09198184
Patent No. 6010859
GENERAL INFORMATION: Jennifer L.
APPLICANT: Gugler, Karl
TITLE OF INVENTION: NOVEL RAB PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY / AGENT INFORMATION:
NAME: Billings, Lucy J.
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/82
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyto
STREET: 3174 Por:
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                     181 SPQGSNQGVKITPDQQ 196
                                                                                                                                                                                                                                                                                                            152 GAEKSNVKIQSTPVKQ 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 47.2%; Score 418; DB 2; L
Similarity 42.9%; Pred. No. 5.5e-41;
84; Conservative 33; Mismatches 47;
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Incyte Pharmaceuticals, Inc
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                                                        Karl
NOVEL RAB PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/824,873
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                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Hlavka,
APPLICANT: Pincus,
APPLICANT: No. 584
                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: SIN
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 234746
                                                                                                                                                                                                        tent No.
                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                           NITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action
                                                             TUMBER OF SEQUENCES:
                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/824,873
                                                                                                                           PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415-855-0555
               STREET:
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                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
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Boulder
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                                                                                                                                                                                                                                                                                                                                                                                                                                  IWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILG 120
                                                                                                                                                                                                                                                                                                                                                                    NKCDVNDKROVSKERGEKLALDYGIKFMETSAKANINVENAFFTLARDIKAKMDKKLEGN 180
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          3: Greenlee and Winner, P.C. 5370 Manhattan Circle, Suite 201
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                                                                                                                                          Pincus, Matthew R. No. 5840683le, John F.
                                                                                                            Kende, Andrew S.
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                                                                                                                          Henry B.
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Pred. No. 5.5e-41;
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Search completed: June 18, 2003, 15:25:01

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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: N
ORIGINAL SOURCE:
ORGANISM: Can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 37 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/531,525
                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                157 NVKIQSTPVKQ 167
                                                                 124 NDKRQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLARDIKAKMDKKLEGNSPQGS 183
184 NOGVKITPDQQ 194
                                                                                                     97
                                                                                                                                      64 AGQERFRTITTAYYRAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILGNKCDV 123
                                                                                                                                                                                                      4 YDYLFKLLLIGDSGYGKTCVLFRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQIWDT
                                                                                                                                                                                                                            8 YDYLFKLLLIGDSGYGKSCLLLRFADDTYTESYISTIGYDFKIRTIELDGKTIKLQI---
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                                                                                                  TTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAGGAEKS 156
                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                            47.1%; Score 417.5; DB 2 43.5%; Pred. No. 6.2e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33,878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37-94
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                              Length 205;
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                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                                                           Gaps
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Title: Perfect score: Sequence:

OM protein -

protein search, using sw

on:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

417779 seqs, 108206813 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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886
1 MSSMNPEYDYLFKLLLIGDS.....EKSNVKIQSTPVKQSGGGCC 173
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: /cgn2_6/ptodata/2/pubpaa/CT_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_RUB_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_RUB_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_RUBCOMB.pep:*
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: /cgn2_6/ptodata/2/pubpaa/US07_RUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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           10 US-09-820-003A-2
10 US-09-820-003A-4
9 US-10-102-806-466
10 US-09-967-736-3
10 US-09-967-736-8
10 US-09-967-736-8
10 US-09-925-300-1571
10 US-09-925-302-534
10 US-09-925-302-534
10 US-09-925-302-534
10 US-09-945-173-5
10 US-09-945-173-5
10 US-09-945-173-5
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10 US-09-764-868-117
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     Sequence 2, Appli
Sequence 466, App
Sequence 3, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 1571, Appli
Sequence 1574, Appli
Sequence 1574, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 77, Appli
Sequence 1117, Appli
Sequence 701, Appli
Sequence 701, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09020003A
; Patent No. US20020142302A1
; GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al.
FITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THE TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001196
CURRENT APPLICATION NUMBER: US/09/820,003A
CURRENT FILIG DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FRASISEQ for Windows Version 4.0
LENGTH: 173
RESULT 2
US-09-820-003A-4
IS-09-820-003A-4
; Sequence 4, Application US/09820003A
; Patent No. US20020142382A1
; GENERAL INFORMATION:
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US-09-820-003A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 173;
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Best Local
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                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Silarity 100.0%; FC Conservative 0;
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9 US-09-764-868-1106
9 US-09-764-868-1106
9 US-09-764-868-1120
10 US-09-764-868-1120
10 US-09-764-868-1120
10 US-09-764-868-1120
10 US-09-764-868-1100
10 US-09-25-307-783
10 US-09-25-307-783
10 US-09-764-868-1112
10 US-09-764-868-1112
10 US-09-764-868-112
10 US-09-764-868-110
10 US-09-988-974-3
10 US-09-988-974-3
10 US-09-988-974-3
10 US-09-988-974-3
10 US-09-988-974-3
10 US-09-763-2884-28
10 US-09-765-2884-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 886; DB 10;
Pred. No. 1.2e-76;
); Mismatches 0;
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Sequence 1106, App
Sequence 1106, App
Sequence 544, App
Sequence 1120, Ap
Sequence 1120, Ap
Sequence 1100, Ap
Sequence 1100, Ap
Sequence 1100, Ap
Sequence 1100, Ap
Sequence 110, Appl
Sequence 1112, Ap
Sequence 1112, Ap
Sequence 692, Appl
Sequence 1077, Ap
Sequence 1177, Ap
Sequence
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Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/Pi
2: /cgn2_6/ptodata/2/pubpaa/Pi
3: /cgn2_6/ptodata/2/pubpaa/Pi
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13: /cgn2_6/ptodata/2/pubpaa/Pi
14: /cgn2_6/ptodata/2/pubpaa/Pi
14: /cgn2_6/ptodata/2/pubpaa/Pi

Result

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60 60 SUMMARIES

Query Match

10 10 11 12 13 14 15 16 16

414 403.5 390.5 390.5 362.5 362.5 362.5 362.5 323 323 323 323 321 321

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                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 466, Appropriation No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver: SEQ ID NO 466
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-0
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/820,003A
CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: CL001196
                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                      82
                                                                        62 LQI-----
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                                                                                                     22 AAMNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIK 81
                                                                                                                           T: MERKULOV, Gennady et al.
INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS.
INVENTION: NUCLEIC ACID MOLECULES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSEMTMAAEIKKRMGPGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSSMNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTI
VGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGAT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGGAEKSNVKIQSTPVKQSGGGCC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESFNNVKQWLQEIDRYASENVNKL 137
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                                  LQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGGAEKSNVKIQSTPVKQSGGGCC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10102806
5. US20030054421A1
                                                                                                                                                                              Conservative
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                                                                                                                                                                                          86.7%;
76.5%;
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                                                                                                                                                                        Score 768.5; DB 9; Pred. No. 2.5e-65; 8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 860; DB 10
Pred. No. 5e-74;
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                                                        -ESFNNVKQWLQEIDRYASENVNKLL 89
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33;
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                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: US-09-967-736-3
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                                                                                                                                                                                                                         Best Loc
Matches
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                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/967,736
FILING DATE: 28-Sep-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/154,602
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: RAB PROTEINS NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
   152
                                  121
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                                                                 92
                                                                                                61
                                                                                                                             64
                                                                                                                                                                                                                           156;
                                                                                                                                                                                          4 MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
                                                                                                                                                                                                                                        Similarity
GAEKSNYKIQSTPYKQSGGGCC
                                                    NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG
                                                                                              IWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLLVG
                                                                                                                                                           MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
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                                                                                                                                                                                                                                                                                                                        CLONE: 2514506
                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatite OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                   LIBRARY:
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                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                         Score 766.5;
Pred. No. 3.3e
6; Mismatches
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                                                                                                                            ESFNNVKQWLQEIDRYASENVNKLLVG
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                                                                                                                                                                                                                         Indels
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G-ERPNLKIDSTPVKPAGGGCC

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RESULT 5
US-09-967-736-8
US-09-967-736-8; Sequence 8, Application US/09967736; Patent No. US20020103340A1; GENERAL INFORMATION:
CHAPPLICANT: Hillman, Jennifer L.
Lal, Preeti
                                                                                                                                                                                                                                                                                                                                            ; LIBRARY: GenBank
; CLONE: 57006
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-967-736-8
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPHONE: 415-85-0556
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: DISMette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FESISED for Windows Version 2.0
SOFTWARE: SESISED: FOR WINDER: US/09/967,736
APPLICATION NUMBER: US/09/967,736
PILING DATE: 28-Sep-2001
PRICATION BATA:
APPLICATION NUMBER: 09/154,602
PILING DATE: OTORKOOWN-
PILING DATE: OTORKOOWN-
PILING DATE: OTORKOOWN-
PILING DATE: OTORKOOWN-
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TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                              152
                                                                92 NKCDLTTKKYVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIKKRMGPGATAG 151
                                                                                                                                 61 IWDTAGQERFRTVTSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLLVG 120
                                                                                                                                                             64 I------BSFUNVKQWLQEIDRYASENVNKLLVG 91
                                                                                                                                                                                                    Similarity 76.2
54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
G-ERPNIKIDSTPVKSASGCC 201
                            GAEKSNVKIQSTPVKQSGGGCC 173
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76.2%;
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RESULT 6
US-09-794-257-8
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APPLICANT: ZHU, Shiaoping et al.

TITLE OF INVERTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVERTION: UCLEBIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVERTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001214

CURRENT APPLICATION UNMEER: US/09/822,860

CURRENT FILING DATE: 2001-04-02

CURRENT FILING DATE: 2001-04-02

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

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PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 16
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 207
TYPEN: DATE

TENTH: 207
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Patent No. US20020009804A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32705, 23224, 27423, 32700,
TITLE OF INVENTION: Buman G-Proteins
TITLE OF INVENTION: Buman G-Proteins
TITLE REFERENCE: 35800/209285
THE REFERENCE: 35800/209285
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
CURRENT FILING DATE: 2001-02-27
CURRENT FILING DATE: 2001-02-27
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Best Local S
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Best Local S:
Matches 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 IWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIKNWIRNIEEHASSDVERMILG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84;
61 GQERERTITTAYYRGAMGIMKVYDITNEKSEDNIKNWIRNIEBHASSDVERMILGNKCDM 120
                                     9 DYLFKLLLIGDSGYGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQI----
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34; Conservative
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                                                                                                                                                                                                                                                                  h 46.6%; Score 413; DB 10; Length 190; Similarity 42.1%; Pred. No. 1.1e-31; 80; Conservative 38; Mismatches 40; Indels 32;
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; ORGANISM: Homo sapiens
US-09-925-300-1571
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US-09-925-300-1571
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SEQ ID NO 1571
LENGTH: 218
                                  SOFTWARE: Pa
                                                                                                                                                                                                                                                       Sequence 534, Application US/09925302
Patent No. US20020044941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
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                                                                                                        APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                    PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
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ITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
      PRT
                                                                                                                                                                                                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                                                              156
                                                                                                                                                                                                                                                                                                                                                                                                                             144 MDDKRVVPKGKGEQIAREHGIRFFETSAKANINIEKAFLTLAEDI--
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                      246
                                                      PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                             ----LRKTPVKEPNSENVDISSGGGVTGWKSKCC
                                                                                                                                                                                                                                                                                                                                                                                            SNVKIQSTPVKQ-----SGGG-----CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDLLFKLLLIGDSGYGKTCYLFRESDDAFNTTFISTIGIDFKIKTYELQGKKIKLQIWDT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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39.7%; Pred. No. 1.1
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               US-09-794-257-16
Sequence 16, Application US/09794257; Patent No. US/0020009804A1; GENERAL INFORMATION:
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Best Local '
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APPLICANT: Meyers, Rachel
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; ORGANISM: Homo sapiens US-09-925-302-534
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US-09-834-765-766
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                                                                                                                                                                                                                                                                                                                                                                    ; NUMBER OF SEQ ID NO; SOFTWARE: FastSEQ f; SEQ ID NO 766; LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT TITLE OF INVENTION: AND DETECTION OF CANCER FILE REFERENCE: 129,60911

CURRENT APPLICATION NUMBER: US/09/834,765

CURRENT FILING DATE: 2001-09-21

PRIOR APPLICATION NUMBER: 60/197,647

PRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mary Faris
APPLICANT: Pia M. Challita-Eid
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                      100 KVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEIK 141
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121 RQVSKERGEKLALDYGIKFMETSAKANINVENAFFTLARDIK 162
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b. US20020055478A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78; Conservative
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                            FKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQI------
                                                                                                                                                      FKLLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQIWDTAGQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steve Chappell Mitchell Daniel E.H. Afar
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                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              for Windows Version 4.0
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45.18;
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Pred. No. 2.2e-29;
35; Mismatches 41
                                                                                                                                                                                                                                Score 371; DB 1
Pred. No. 9e-28;
8; Mismatches
                                                                                                              -----ESFNNVKQWLQEIDRYASENVNKLLVGNKCDLTTK 99
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APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 47324, A NOVEL HUMAN G-PROTEIN AND USE
TITLE OF INVENTION: THERREFOR
FILE REFERENCE: 381.55-20035.00
CURRENT APPLICATION NUMBER: US(709/945,173
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,293
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTLSEQ FOR WINDOWS VETSION 4.0
SEQ ID NO 5
LENGTH: 198
TYPES: DEM
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US-09-945-173-5
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                                                                                                                                                       Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09945173
Patent No. US20020127568A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
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Best Local :
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FILE REFERENCE: 35800/20928
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/185,606
PRIOR FILING DATE: 2000-02-29
NUMBER. OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 198
                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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61 FRALRPAYYRGAQGFLLVYDITSRDSFENVKKWLEEILRHADKDENVPIVLVGNKCDLED 120
                                                                                                                                                Ch 40.9%; Score 362.5; DB 10; Length 198; I Similarity 41.7%; Prod. No. 7.4e-27; B6; Conservative 25; Mismatches 40; Indels 55;
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Similarity 41.7%;
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Pred. No. 7.4e-27;
5; Mismatches 40; Indels 55;
                                 ----ESFNNVKQWLQEIDRYA--SENVNKLLVGNKCDLT-
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Sequence 67, Application US/09350874

Patent No. US20020019020A1

GENERAL INFORMATION:
APPLICANT: Rhodes, Kenneth
APPLICANT: AND Wengian

TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
FILE REFERENCE: MNI-059
CURRENT APPLICATION NUMBER: US/09/350,874
CURRENT FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: USSN 60/110,277
EARLIER FILING DATE: 1998-11-30
EARLIER APPLICATION NUMBER: USSN 60/110,033
EARLIER APPLICATION NUMBER: USSN 60/109,333
EARLIER APPLICATION NUMBER: USSN 60/109,333
EARLIER APPLICATION NUMBER: USSN 60/109,333
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Patent No. US20020150916A1

GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
ITILE OF INVENTION: 47316, A NOVEL HUMAN G-PROTEIN AND USES
ITILE OF INVENTION: THEREFOR
ITILE OF INVENTION: THEREFOR
ITILE OF INVENTION: US/09/972,529
CURRENT APPLICATION NUMBER: US/09/972,529
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/237,716
PRIOR PILING DATE: 2000-10-05

PRIOR FILING DATE: 2000-10-05

SOSTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

TENCENT 10
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US-09-350-874-67
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US-09-972-529-4
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EARLIER FILING DATE: 1998-11-20
EARLIER APPLICATION NUMBER: USSN 09/298,731
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178
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Search completed: June 18, 2003, 15:24:31 Job time: 33 secs
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US-09-817-198A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09817198A
Patent No. US20020146758A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 212
TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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LENGTH: 212
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NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
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                                                                               181 RTCASNELALAELEEDEGKTEG 202
                                                                                                                        148 ATAGGAEKSNVKIQSTPVKQSG 169
                                                                                                                                                              121 NKADEEOKROVGREOGOOLAKEYGMDFYETSACTNLNIKESFTRLTELVLOAHRKELDGL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 LESRREVKKEEGEAFAREHGLIFMETSAKTASNVEEAFINTAKEIYEKIQEGVFDINNEA 182
                                                                                                                                                                                                       92 NKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATNVEQSFMTMAAEI----KKRMGPG 147
                                                                                                                                                                                                                                              61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                             1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 4.6e-23;
6; Mismatches 61;
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Command line parameters:

-MODEL-frame+_D2n.model -DEV=xlp
-MODEL-frame+_D2n.model -DEV=xlp
-Q-/cgn2_1/USFTO_Spool/US99820003/runat_18062003_144132_13246/app_query.fasta_1.327
-DB-Published_Applications_NA -QFMT-fastap -SUFFIX-p2n.rnpb -MINMATCH=0.1
-LOOPEXPO -LOOPEXPO -UNITS-blts -START=1 -END-1 -MATRIX-blosum62
-TRANS-humand0.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0
-MAXLEN-200000000 -USER-US09820003_eCGN_11_80_erunat_18062003_144132_13246
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-LONGLOG -DEV_TIMEDUT=120 -WARNI_TIMEDUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5
-FGAPDP=6 -FGAPEXT=7 -YGAPDP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
            886
768.5
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1: //cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: //cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: //cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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5: //cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

6: //cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: //cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: //cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

9: //cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

10: //cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

11: //cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

11: //cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13: //cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

14: //cgn2_6/ptodata/2/pubpna/US0_NEW_PUB.seq:*
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Match Length DB
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(without alignments)
1839.601 Million cell updates/sec
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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      1405 10 US-09-820-003A-1
925 10 US-09-967-736-4
939 9 US-10-102-806-48
609 9 US-09-938-842A-832
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Sequence 1, Appli
Sequence 4, Appli
Sequence 48, Appl
Sequence 832, App
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                               Best Local Similarity:
Query Match:
DB:
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equence 91, quence 487, quence 66, equence 10, quence 346, equence 11, quence 11, equence 12, equence 13, equence 270, quence 270, quence 201, quence 48, quence 48, quence 48, quence 49, quence 48, quence 48,	US-09-925-302-91 US-09-919-36-87 US-09-919-36-87 US-09-919-36-87 US-10-37-270-646 US-09-817-1980A-1 US-09-918-95-20 US-09-918-95-20 US-09-918-95-270 US-09-918-95-270 US-09-918-95-270 US-09-918-95-270 US-09-918-95-274-36 US-09-918-95-274-36 US-09-918-95-274-36 US-09-918-95-274-36 US-09-918-95-274-36 US-09-918-95-274-36 US-09-918-9172-49 US-09-918-9172-49 US-09-764-868-79 US-09-764-868-79 US-09-764-868-498 US-09-764-868-498 US-09-764-868-507 ALIGNMENTS ALIGNMENTS OOOJA OOOJA	110 10 10 10 10 10 10 10 10 10 10 10 10	1274 1274 1069 1069 1069 1069 1069 1069 1069 1069	0.5 44.1 36.4 41.1 34.4 38.8 34.3 38.7 3.4.3 38.7 3.5 38.7 3.5 38.7 3.5 37.0 7.5 37.0 7.5 37.0 3.6 3.6 3.6 3.2 3.6 3.6 3.6 3.2 3.6	RECE NO. 1 30.5 30.5 30.5 30.5 30.5 30.5 30.5 30.5	16 3 1 1 1 1 3 2 1 1 1 1 1 1 1 1 1 1 1 1 1
Sequence 529, Appli Sequence 36, Appli Sequence 836, Appli Sequence 99, Appli Sequence 7, Appli Sequence 79, Appli Sequence 815, App Sequence 894, App Sequence 894, App Sequence 631, App	US-09-770-445-529 US-09-820-003A-3 US-09-820-003A-36 US-09-938-842A-836 US-09-938-842A-836 US-09-949-95-7-7 US-09-949-975-87 US-09-834-975-886 US-09-834-975-886 US-09-834-975-886 US-09-834-975-886 US-09-834-975-886	7771100	4605 605 655 657 116 249 249 249 249		619.5 487.5 481 428.5 414 414 414 414 414 414	114 112 114 114 115

DB:	Query Match:	Best Local Similarity:	=	Score:	Pred. No.:	Alignment Scores:		US-09-820-003A-1	; ORGANISM: Homo sapien	; TYPE: DNA	; LENGTH: 1405	1 1 1 1 1 1 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09967736 Patent No. US20020103340A1 GENERAL INFORMATION:
                APPLICATION NUMBER: 09/154,602
FILING DATE: CODKNOWN>
ATTORNEY_AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367
TELECOMMUNICATION INFORMATION:
                                                                                                                                                           ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Ve

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Dr.
                                                                                                                       PRIOR
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                                                                                                                    APPLICATION NUMBER: US/09/967,736 FILING DATE: 28-Sep-2001 APPLICATION DATA:
                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValValAspTyrThrThrAlaLysGluPheAlaAspSerLeuGlyIleProPheLeuGlu
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                                                                                                                                                                                                                                                                                                                                                                     Shah, Purvi
OF INVENTION: RAB PROTEINS
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Shah, Purvi
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Query Match:
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Sequence 48, Application US/101
Publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                   GlyGlyCysCys
                                                                                                                                                                              AlaGlyGlyAlaGluLysSerAsnValLysIleGlnSerThrProValLysGlnSerGly 169
                                                                                                                                                                                                                                    GluGlnSerPheMetThrMetAlaAlaGluIleLysLysArgMetGlyProGlyAlaThr
                                                                                                                                                                                                                                                                                              PheAlaAspSerLeuGlyIleProPheLeuGluThrSerAlaLysAsnAlaThrAsnVal 129
                                                                                                                                                                                                                                                                                                                                                         ValGlyAsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLysGlu
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                                                                                                                                                               TCTGGGGGC---
                                                                                                                                                                                                                        GAGCAGGCGTTCATGACCATGGCTGCTGAAATCAAAAAGCGGATGGGGCCTGGAGCAGCC
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CLONE: 2514506
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76.47%
86.74%
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Matches:
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179 41 119 21

599 149

; NAME/KEY: misc_feature ; LOCATION: (937) ; OTHER INFORMATION: n equals a,t,g, or c US-10-102-806-48

ORGANISM: Homo sapiens FEATURE:

CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0

CURRENT FILING DATE: 2002-03-22

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA103P1C1

SEQ ID NO 48 LENGTH: 93

939

TYPE: DNA

Alignment Scores:

Query Match:

Best Local Similarity: Percent Similarity:

80.39% 76.47% 86.74% 9

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

939 156

US-09-820-003B-2 (1-173) x US-10-102-806-48 (1-939)

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150 AlaGlyGlyAlaGluLysSerAsnValLysIleGlnSerThrProValLysGlnSerGly 165
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                                                                                                                604 TCTGGGGGC---GAGCGGCCCAATCTCAAGATCGACACCCCCTGTAAAGCCGGCTGGC
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US-09-938-842A-832
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CURRENT REPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/221,866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DA
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                                                                                                421 GATGAACTTGGGATCCCATTCTTGGAAACAAGTGCTAAGAATGCTACCAATGTCGAAGAA 480
                                                                                                                                                112 AspSerLeuGlyIleProPheLeuGluThrSerAlaLysAsnAlaThrAsnValGluGln 131
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132 SerPheMetThrMetAlaAlaGluIleLysLysArgMetGlyProGlyAlaThrAlaGly 151
                                                                                                                                                                                                                                                                            361 AACAAGTGTGATCTCACATCACAGAAAGTTGTATCCACTGAGACAGCTAAGGCTTTCGCT 420
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US20020160378A1
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170 GlyGlyCysCys 173

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APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: Fastser
                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Arabidopsis thaliana US-09-770-445-529
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US-09-770-445-529
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LENGTH: 881
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63
                                                          43
                                                                                                     23 GlyLysSerCysLeuLeuLeuArgPheAlaAspAspThrTyrThrGluSerTyrIleSer
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                                                                                                                                                  US20020023281A1
                                            ThrIleGlyValAspPheLysIleArgThrIleGluLeuAspGlyLysThrIleLysLeu
                                                                                       GGCAAGTCTTGTCTTTTTGAGATTCTCTGATGATTCTTATGTAGAAAGTTACATTAGC
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Hamilton, Carol M
Price, Jennifer L
Raines, Tracy M.
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Slader, Ted
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Woessner, Jeffrey P.
Haas, William David
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Rameaka, Joshua G.
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                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001196
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 3
LENGTH: 46050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/820,003A CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(46050)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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            42842 TTTCAAATGTCTTTT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 LysGlnTrpLeuGlnGluIleAspArgTyrAlaSerGluAsnValAsnLysLeuLeuVal
                                       44 IleGlyValAspPheLysIleArgThrIleGluLeuAspGlyLysThrIleLysLeuGln
                                                                                                  24 LysSerCysLeuLeuLeuArgPheAlaAspAspThrTyrThrGluSerTyrIleSerThr
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                                                                       AGGTCAGGAACGATGTTTCTGTTTATTCCAGAACTATATTATCGAACTATATTATCAGTC
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Sequence 36, Application US/09820003A
PRICENT NO. US20020142382A1
GENERAL INFORMATION:
APPLICANT: MERKULOY, Gennady et al.
TITLE OF INVENTION: SOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001196
CURRENT APPLICATION NUMBER: US/09/820,003A
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID MOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 601
                                                             US-09-820-003B-2 (1-173) x US-09-820-003A-36 (1-601)
                                                                                                          Query Match:
                                                                                                                                                                    Alignment Scores: Pred. No.:.
                                                                                                                                                                                                                  ; ORGANISM: Homo sapien
US-09-820-003A-36
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US-09-820-003A-36
                                                                                                                      Percent Similarity:
Best Local Similarity:
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     ThrSerAlaLysAsnAlaThrAsnValGluGlnSerPheMetThrMetAlaAlaGluIle 140
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54.29%
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                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                 ; LENGTH: 651
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-836
                                                                                                                                                                                           APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT PILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEG ID NO 836
LENGTH: 651
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US-09-938-842A-836
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US-09-820-003B-2 (1-173) x US-09-938-842A-836 (1-651)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 836, Application US/09938842A Patent No. US20020160378A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
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                                                                                      ; ORGANISM: homo sapiens US-09-794-257-9
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                                  Percent Similarity:
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SOFTWARE: FastSEQ for W
SEQ ID NO 9
LENGTH: 624
TYPE: DNA
                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 32705, 23224, 27423,
TITLE OF INVENTION: Human G-Proteins
FILE REFERENCE: 35800/209285
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
                                                                                                                                                                                                                                                         Sequence 9, Application US/09794257 Patent No. US20020009804A1
                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/185, PRIOR FILING DATE: 2000-02-29
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Best Local Similarity:
Query Match:
                              Score:
                                                                        ; NAME/KEY: CDS
; LOCATION: (18)...
US-09-794-257-7
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                                          Pred. No.:
                                                    Alignment
                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 7
                                                                                                        TYPE: DNA
ORGANISM: homo
FEATURE:
                                                                                                                                                                              PRIOR FILING DATE: 2000-02-29
                                                                                                                                        LENGTH:
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301 AATTGGATCAGAAACATTGAAGAGCATGCCTCTTCCGATGTCGAAAGAATGATCCTGGGT
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US-09-834-975-879
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                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFFWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 879
LENGTH: 2497
                                                                                                                                                                                                                                                   APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Bolt, Andrew
APPLICANT: Wan Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILLING DATE: 2001-04-13
CURRENT FILLING DATE: 2001-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 879, Application US/09834975 Patent No. US20020110815A1
                           NAME/KEY: misc_feature LOCATION: (1)...(2497) OTHER INFORMATION: n = -09-834-975-879
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lillie, James
                                                                                                      FEATURE:
                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 885
LENGTH: 2497
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                   APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Wan Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS
TITLE OF INVENTION: FOR THE IDENTIFICATION, A
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
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; LOCATION: (1)...(2497)
; OTHER INFORMATION: n =
US-09-834-975-885
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                                                                                                                                                                  Sequence 894, Application Patent No. US20020110815A1
                                              APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, I
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
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Sequence 896, Application US/09834975
Patent NO. US20020110815A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Bolt, Andrew
APPLICANT: Non Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS ASTITLE OF INVENTION: FOR THE IDENTIFICATION, AS:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 894
LENGTH: 2497
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TYPE: DNA
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RESULT 15
US-09-925-300-631
Sequence 631, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
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; LOCATION: (1)...(2497)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-820-003B-2 (1-173) x US-09-834-975-896 (1-2497)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION UNUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 896
LENGTH: 2497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: OF FILE REFERENCE: MRI-016E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                             132 SerPheMetThrMetAlaAlaGluTle------LysLysArgMetGlyProGly 147
                                                                                                                                                                                                                                                                                                                                          512 ATTGACTATGGGATTAAATTCTTGGAGACAAGCGCAAAATCCAGTGCAAATGTAGAAGG 571
                                                                                                                                                  632 AATTCAGCAGGAGCAGGT-----GGACCAGTGAAAATAACAGAAAA-CCGATCAAAGAA 684
                                                                                                                                                                                               148 AlaThrAlaGlyGlyAlaGluLysSerAsnValLysIleGlnSerThrProValLysGln 167
                                                                                                                                                                                                                                                                                                                                                                                          112 AspSerLeuGlyIleProPheLeuGluThrSerAlaLysAsnAlaThrAsnValGluGln 131
                                                                                                                                                                                                                                                                                                                                                                                                                                          452 AACAAATGTGATATGAATGACAAAAGACAAGTGTCAAAAGAAGAAGGGGGAGAAGCTAGCA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 AATTGGATCAGAAACATTGAAGAGCATGCCTCTTCCGATGTCGAAAGAATGATCCTGGGT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 GCCATGGGCATTATGCTGGTCTATGACATCACAAATGAAAAATCCTTTGACAATATTAAA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 ATATGGGACACAGCGGGTCAGGAAAGATTCCGAACAATCACGACAGCGTACTACAGAGGA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 AAGACCTGCCTCCTGTTCCGCCTTCTCAGAGGACGCCTTCAACCACCTTCATCTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 IleGlyValAspPheLysIleArgThrIleGluLeuAspGlyLysThrIleLysLeuGln 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 AsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLysGluPheAla 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 GlnTrpLeuGlnGluIleAspArgTyrAlaSerGluAsnValAsnLysLeuLeuValGly 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 -----GluSerPheAsnAsnValLys 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 LysSerCysLeuLeuLeuArgPheAlaAspAspThrTyrThrGluSerTyrIleSerThr 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 ATGGCGAAGACGTACGATTATCTCTTCAAGCTCCTGCTGATCGGCGACTCGGGGGTAGGC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 MetAsnProGluTyrAspTyrLeuPheLysLeuLeuLeuIleGlyAspSerGlyValGly 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.06e-43
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: n equals a,t,g, or US-09-925-300-631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 631
LENGTH: 1537
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
NAME/KEY: misc feature LOCATION: (5)
                                               1043 -----CTTCGAAAGACCCCTGTAAAAGAGCCCAACAGTGAAAATGTAGATATC 1090
                                                                                                                                               1028 TTAGCTGAAGATATC----- 1042
                                                                                                                                                                                       136 MetAlaAlaGluIleLysLysArgMetGlyProGlyAlaThrAlaGlyGlyAlaGluLys 155
                                                                                                                                                                                                                                                                116 IleProPheLeuGluThrSerAlaLysAsnAlaThrAsnValGluGlnSerPheMetThr 135
168 ---SerGlyGlyGly-----CysCys 173
                                                                                             968 ATTAGGTTTTTTGAGACTAGTGCAAAAGCAAATATAAACATCGAAAAGGCGTTCCTCACG 1027
                                                                                                                                                                                                                                                                                                                                       908 ATGGACGACAAAAGAGTTGTACCTAAAAGGAAAAAGGAGAACAGATTGCAAGGGAGCATGGT 967
                                                                                                                                                                                                                                                                                                                                                                                                                                    848 AACATAGATGAGCATGCCAATGAAGATGTGGAAAGAATGTTACTAGGAAACAAGTGTGAT 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              608 CTTTTTCGTTTTTCGGATGATGCCTTCAATACTACCTTTATTTCCACCATAGGAATAGAC 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      548 TACGACCTGCTTTTCAAGCTGCTCCTGATCGGGGATTCCGGAGTGGGGAAGACCTGCGTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 GluIleAspArgTyrAlaSerGluAsnValAsnLysLeuLeuValGlyAsnLysCysAsp 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    788 ATGCTAGTATATGACATCACCAATGGTAAAAGTTTTGAAAACATCAGCAAATGGCTTAGA 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 728 GCAGGCCAGGAGCGATTTCACACCATCACAACCTCCTACTACAGAGGCGCAATGGGTATC 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 PheLysIleArgThrIleGluLeuAspGlyLysThrIleLysLeuGlnIle----- 64
                                                                                                                                                                                                                                                                                                                                                                                    96 LeuThrThrLysLysValValAspTyrThrThrAlaLysGluPheAlaAspSerLeuGly 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 -----GluSerPheAsnAsnValLysGlnTrpLeuGln 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ----- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 LeuLeuArgPheAlaAspAspThrTyrThrGluSerTyrIleSerThrIleGlyValAsp 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 TyrAspTyrLeuPheLysLeuLeuIleGlyAspSerGlyValGlyLysSerCysLeu 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.46e-42
403.50
54.67%
39.72%
45.54%
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Indels:
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Search completed: June 22, 2003, 19:48:03 Job time: 154 secs.

Run

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Command line parameters:

-MODEL-framet_p2n.model -DEV=xlp
-MODEL-framet_p2n.model -DEV=xlp
-O_-Cgn2_1_VBFTO_Spool_VBS9820003/runat_18052003_144130_13134/app_query.fasta_1.327
-OB-Issued_Patents_NA -QFMT-fastap -SUFFIX-p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-blts -START=1 -END=-1 -MATKIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALLGH=200 -TMR_SCORE-pct -THR_MAX-100 -TRR_MIN-0 -ALIGN=15
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-NO_MMAP -LARGEDUERY -NGE_SCORES-0 -WAIT -DSPBLCCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                        Result
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       768.5
768.5
333
314.5
314.5
282.5
282.5
282.5
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282.5
                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_NA:*

1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

5: /cgn2_6/ptodata/1

5: /cgn2_6/ptodata/1
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                Match
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886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
/cgn2_6/ptodata/1/lna/5B_COMB.seq:*
/cgn2_6/ptodata/1/lna/6B_COMB.seq:*
/cgn2_6/ptodata/1/lna/6B_COMB.seq:*
/cgn2_6/ptodata/1/lna/FGNE_COMB.seq:*
/cgn2_6/ptodata/1/lna/FGNE_COMB.seq:*
                                                                                                                                                                                                                                                                                                Length DB
          2612
1340
1340
847
848
607
5775
  US-08-916-901-4
US-09-154-602-4
US-09-399-913-68
US-09-888-077A-28
US-09-888-9708-142
US-09-484-9708-142
US-09-198-184-2
US-09-198-184-2
US-08-741-411-2
US-08-429-964-85
US-08-306-6918-15
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7.0
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828.986 Million cell updates/sec
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appl
Sequence 28, Appl
Sequence 14, Appl
Sequence 14, Appli
Sequence 2, Appli
Sequence 15, Appli
                                                                                                                                                                                                                                                                              Description
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45	44	43	42	41	40	9	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	
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1098	1098	1098	2713	2713	1058	1058	591	591	624	5197	1074	1074	914	779	1533	1172	1255	1407	450	820	168	890	1749	480	1175	4480	2436	570	570	803	574	5775	
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-09-368-402-	-09-193-510-	8-948-616-	-09-154-602-	-08-916-901-	-09-387-341-	-09-156-807-	-09-387-34	-09-156-979-	-09-415-522-	-09-293-170-	-09-387-341-	-09-156-424-	8-773-423-	-08-766-551-	-09-075-454-	-09-075-454-	-08-766-551-	9-493-914-1	-08-884-866A	-08-741-411-6	9-328-11	-08-741-411	-09-149-476	-08-884-866A-	S-08-773-423-6	-09-167-322-1	S-08-306-691B-	-08-884-866A-	8-884-866A-	-09-075-454-1	-429-964-	51-	
, Appl	6, Appl	6, Appl	6, Appl	6, Appl	109, Ap	1, Appl	Sequence 68, Appl	1, Appl	1, Appl	6, Appl	1, Appl	1, Appl	2, Appl	4, Appl	1, App	8, Appl	6, Appl	1, Appl	0, App	6, Appl	222, Ap	4	54, App	9, Appl	6, Appl	12, App	e 16, App	e 11, App	e 2, Appl	3, App	83, App	29, App	

ALIGNMENTS

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US-08-916-901-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/08916901
; Patent No. 5892012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
            FILING DATE:

ATTORNEY/AGENT INFORMATION:

ATMANE: BILLINGS, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                              STREET: 317.
CITY: Palo Alto
STATE: CA
TCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                          94304
415-845-4166
                                                                                                                                                                                                                                                                                                                                  Diskette
                                                              PF-0367 US
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                      RESULT 2
US-09-154-602-4
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Pred. No.:
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                                   Sequence 4, Application US/09154602 Patent No. 6300472 GENERAL INFORMATION:
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 APPLICANT:
APPLICANT:
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LIBRARY: LIVRTUTO4
CLONE: 2514506
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                                                                                                                      GlyGlyCysCys 173
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                                                                                                                                                                       AlaGlyGlyAlaGluLysSerAsnValLysIleGlnSerThrProValLysGlnSerGly
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                                                                                                           GGTGGCTGTTGC
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Hillman, Jennifer
Lal, Preeti
Corley, Neil C.
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Best Local Similarity:
Query Match:
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US-09-154-602-4
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INFORMATION FOR SEQ ID NO:
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LIBRARY: LIVRT
CLONE: 2514506
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TITLE OF INVENTION: RAB
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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CITY: Palo Alto
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                      ValLysGlnTrpLeuGlnGluIleAspArgTyrAlaSerGluAsnValAsnLysLeuLeu
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US-09-820-003B-2 (1-173) x US-09-399-913-66 (1-639) Qy 8 TyrAspTyrLeuPheLysLeuLeuLeuLeuIleGlyAspSerGlyValGlyLysSerCysLeu 27	Alignment Scores: Pred. No.: 2.52e-36 Score: 333.00 Matches: 73 Percent Similarity: 52.86% Best Local Similarity: 34.76% Query-Match: 37.58% Gaps: 2 Length: 639 Marches: 73 Conservative: 38 Mismatches: 55 Query-Match: 4.66bs: 4.66aps: 2	IENGTH: 639 ITPE: DNA ORANISM: Rattus sp. FEATURE: NAME/KEY: CDS LCCATION: (1)(636) US-09-399-913-66			ENCE PLICE	; bequence ob, Application US/U9399913 ; Patent No. 6361971 ; GENERAL INFORMATION: ; APPLICANT: Rhodes, Kenneth ; APPLICANT: Betty, Maria ; APPLICANT: Ling, Huai-Ping ; APPLICANT: Nendan	557 GGTGGCTGTTGC	::: :::	QY 130 GLUGLISETPIRMECTINTMECKALARIAGIUI ILELYSLYSAKIGMEGIYPTOGIYALATIN 149		Qy 90 ValGlyAsnLySCySAspLeuThrThrLySLySValValAspTyrThrThrAlaLySGlu 109
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/592,541 FILING DATE: 26-JAN-1996 ATTORNEY/AGENT INFORMATION: NAME: PALISI, THOMAS M REGISTRATION NUMBER: 36,629 REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 654-5000	CLARSIFICATION: 330-0 COMPUTER: RICHARD disk CONFUTER: IIBM PC COMPAtible CONFUTER: IBM PC COMPAtible COMPUTER: OCCUPATION: OCCUPATION	CORRESSE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK STREET: 600 SOUTH AVENUE WEST CITY: WESTFIELD STATE: NJ COUNTRY: USA ZIE: 07090-1497	HOACH BOACH	Qy 166LysGlnSerGlyGlyGlyCysCys 173 ::: :::	Qy 156 SerAsnValLysIleGlnSerThrProVal	427 CITATCITCATGAAACITCTGCAAGACTGCTTCTAATGAAGAGGAGGCATTTAATAAC CTTATCITCATGGAAACITCTGCAAGACTGCTTCTAATGAAGAGGAGGAGGATTTAATAAC 136 MetalaalaGluIleLysLysArgMetGlyProGlyAalaThralaGlyGlyAlaGluLys 110	Oy beuthrthriyslysvalvalAspTyrThrThrAlalysGlubhaAlaAspSerLeuGly 115	GluIl ::: GACGC		QY 64	Qy 48 PheLysIleArgThrIleGluLeuAspGlyLysThrIleLysLeuGlnIle 64

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OTHER INFORMATION: /note=

US-08-888-077A-28
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Best Local Similarity:
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             Sequence 10, Application US/09075454 Patent No. 6391580 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 28:
 APPLICANT:
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                                                                                                                                      GlnSerThrProValLysGlnSerGlyGlyGlyCysCys 173
                                                                                                                                                                                                                                                                                               GCTTTTGCAGAAAAGAATGGTTTGTCATTCATTGAAACTTCGGCCCTAGACTCTACAAAT
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                                                                                                                                                                                                  MetGlyProGlyAlaThrAlaGlyGlyAlaGluLysSerAsnVal------LysIle 160
                                                                                                                                                                                                                                                               ValGluGlnSerPheMetThrMetAlaAlaGluIle------LysLysArg 143
                                                                                                                                                                                                                                                                                                                                                            CTTGTGGGCAATAAGAGTGATCTACGTCATCTCAGGGCAGTTCCTACAGATGAAGCAAGA 473
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Hillman,
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319.00
52.11%
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 Jennifer L.
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Conservative:
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Best Local Similarity:
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APPLICATION NUMBER: 08/766
FILING DATE: DECEMBER 12,
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: UCMCL5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 875 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Batra, Sajeev
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: RAS PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: Herewi
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
             243
                                                                         183
                                                                                                                                    123
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                                                                                                                                                                     25
                                                                                                                                                                                                63 AGTCCGAGCTACGACCTCACGGGCAAGGTGATGCTTCTGGGAGACACAGGCGTCGGCAAA
                                                                                                IleGlyValAspPheLysIleArgThrIleGluLeuAspGlyLysThrIleLysLeuGln
                                                                                                                                    ACATGTTTCCTGATCCAATTCAAAGACGGGGCCTTCCTGTCCGGAACCTTCATAGCCACC
                                                                                                                                                                                                                 AsnProGluTyrAspTyrLeuPheLysLeuLeuLeuIleGlyAspSerGlyValGlyLys:::||| ||||||
                                                                         GTCGGCATAGACTTCAGGAACAAGGTGGTGACTGTGGATGGCGTGAGAGTGAAGCTGCAG
                                                                                                                                                                 SerCysLeuLeuLeuArgPheAlaAspAspThrTyr---ThrGluSerTyrIleSerThr 43
           ATCTGGGACACCGCTGGGCAGGAACGGTTCCGAAGCGTCACCCATGCTTATTACAGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                         1528559
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Corley, Neil C.
Patterson, Chandra
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Lal, Preeti
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Matches:
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RESULT 6
US-09-484-970B-142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:

: NAME/KEY: misc_feature

: OTHER INFORMATION: Incyte ID No. 6426186 412477.1CB1

US-09-484-970B-142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL PROGram
SEQ ID NO 142
LENGTH: 2612
TYPE: Non
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Patent No. 6426186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael
TITLE OF INVENTION: BONE RE
FILE REFERENCE: PB-0014 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                               142 ACATGTTTCCTGATCCAATTCAAAGACGGGGCCTTCCTGTCCGGAACCTTCATAGCCACC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           543 GCCTTTCTGGCCATCGCCAAGGAACTGAAATACCGGGCCGGG 584
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                              322 GCTCAGGCCTTGCTTCTGCTGTATGACATCACCAACAATCTTCTTTCGACAACATCAGG 381
                                                                                                                                                                                                                    202 GTCGGCATAGACTTCAGGAACAAGGTGGTGACTGTGGATGGCGTGAGAGTGAAGCTGCAG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 AACAAGGCGGATATGAGCAGCGAAAGAGTGATCCGTTCCGAAGACGGAGAGACCTTGGCC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 GCCTGGCTCACTGAGATTCATGAGTATGCCCCAGAGGGACGTGGTGATCATGCTGCTAGGC 422
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                                                                                                                         262 ATCTGGGACACCGCTGGGCAGGAACGGTTCCGAAGCGTCACCCATGCTTATTACAGAGAT 321
                                                            65 ------GluSerPheAsnAsnValLys 71
                                                                                                                                                                        64 Ile----- 64
                                                                                                                                                                                                                                                                44 IleGlyValAspPheLysIleArgThrIleGluLeuAspGlyLysThrIleLysLeuGln 63
                                                                                                                                                                                                                                                                                                                                                        25 SerCysLeuLeuLeuArgPheAlaAspAspThrTyr---ThrGluSerTyrIleSerThr 43
                                                                                                                                                                                                                                                                                                                                                                                                          82 AGTCCGAGCTACGACCTCACGGCAAGGTGATGCTTCTGGGAGACACAGGCGTCGGCAAA 141
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314.50
56.90%
35.06%
35.50%
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Matches:
Conservative:
Mismatches:
Indels:
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US-08-824-873-2
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                                            US-09-820-003B-2 (1-173) x US-08-824-873-2 (1-1340)
                                                                                                                      Query Match:
                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                         US-08-824-873-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 1340 base pai
                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: PANCN
CLONE: 738957
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/8:
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Guegler, Karl
TITLE OF INVENTION: NOVE
NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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8 TyrAspTyrLeuPheLysLeuLeuIleGlyAspSerGlyValGlyLysSerCysLeu 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1340 base pairs
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31.88%
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RESULT 8
US-09-198-184-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBL
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for W
 ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Guegler, Karl
TITLE OF INVENTION: NOVEL RAB PROTEIN
                                    FILING DATE:
                                                                                       CLASSIFICATION:
                                                                                                     FILING DATE
                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uGlyIleProPheLeuGluThrSerAlaLysAsnAlaThrAsnValGluGlnSerPheMe 134
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Karl
                                                      08/824,873
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 Sequence
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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                                                                                                  nSerGlyGlyGly-----CysCys 173
                                                                                                                                                                                                                           GGACTCTGCCCATGAGCGTGTGGTGAAGAGGGAGGACGGGGAGAAGCTGGCCAAGGAGTA
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Application US/08773423
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                                                                                                                                                                      uLysSerAsnValLysIleGlnSerThrPro---
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CR: PF-0240
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Matches:
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US-09-820-003B-2 (1-173) x US-08-773-423-4 (1-847)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 847 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5869291
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
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OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,423
FILING DATE: Herewith
FILING DATE: HEREWITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL RAB PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-845-4166
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                                       272 ACAGCTGGCCTGGAGCGGTACCGAGCCATCACCTCGGCGTACTATCGTGGTGCAGTGGGG 331
                                                                                                                   212 GAGTTCTCCACCCGCACTGTGATGTTGGGCACCGCTGCTGTCAAGGCTCAGATCTGGGAC 271
                                                                                                                                                                                               152 CTACTCTCCCGATTCACGCGCAATGAGTTCAGCCACGACAGCCGCCACCACCATCGGGGTT 211
                                                                                                                                                      47 AspPheLysIleArgThrIleGluLeuAspGlyLysThrIleLysLeuGlnIle---- 64
                                                                                                                                                                                                                                    27 LeuLeuLeuArgPheAlaAspAspThrTyrThrGluSerTyrIleSerThrIleGlyVal 46
                                                                                                                                                                                                                                                                           92 GATTATAACTTTGTCTTCAAGGTGGTGCTGATCGGCGAATCAGGTGTGGGGAAGACCAAT 151
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-GluSerPheAsnAsnValLysGlnTrpLeu 74
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US-08-741-411-2
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                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 848 base pairs
                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION UNMER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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APPLICANT: Bandma
APPLICANT: Au-You
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: Herewith CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA
APPLICATION NUMBER: UPPLICATION NUMBER: UPPLICATION NUMBER: UPPLICATION DATA
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION: NOVEL RAB PROTEINS
NUMBER OF SEQUENCES: 12
                                       IMMEDIATE SOURCE:
                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                         TOPOLOGY:
                                                                                              STRANDEDNESS:
                                                                                                                     TYPE:
                                                                                                                                                                                             TELEX:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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                  LIBRARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572 ACTGTCCTGAAAGAAATCTTTGCGAAGGTGTCCAAGCAGAGACAGAACAGCATCCGGACC 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512 GGACTGCTCTTCCTGGAGACCTCAGCCCTGGACTCTACCAATGTTGAGCTAGCCTTTGAG 571
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Consensus
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; Sequence 85, Application US/08429964

; Patent No. 5962243
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                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: BROWN,
APPLICANT: GOLDSTI
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
                                                                                                                                 APPLICANT: REISS, YUVAL
APPLICANT: JAMES, GV L.
TITLE OF INVENTION: METHODS FOR THE IDENTI-
TITLE OF INVENTION: TRANSFERASE INHIBITORS
UNBER OF SEQUENCES: 85
                                                     COUNTRY:
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                                           77210
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                                                                                                                                                                                                                                                                                                                                      GlnSerGlyGlyGlyCysCys 173
                                                                                                                                                                                                                                                                                                                                                                 TTGGACCCCCATGAAAATGGAAACAATGGAACAATCAAAGTTGAGAAG----CCAACCATG 740
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                                                                                                                                                                                                                                                                                                             CAAGCCAGCCGCCGGTGCTGT 761
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                                                                                                                                                                                                     GOLDSTEIN, JOSEPH L.
                                                                                                                                                                                                                   BROWN, MICHAEL S.
                                                     UNITED STATES
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231.50
45.45%
28.34%
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Conservative:
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TOPOLOGY: 11r
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                         307
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US-09-820-003B-2 (1-173) x US-08-429-964-85 (1-607)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: UT TELECOMMUNICATION INFORMATION: TELEPHONE: (712) 418-3000 TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION UNMBER: US 08/021,625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/510,706 FILING DATE: 18-APR-1990 (ABANDONED) CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20-NOV-CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-APR-1991 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                   127 CAAGTAGTAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGACACAGCAGGTCAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                              52 ThrIleGluLeuAspGlyLysThrIleLysLeuGlnIle----
                                                                                                                                                                                                                                                                                                                                              70 ATTGACAATCATTTTGTGGACGAATATGATCCAACAATAGAGGATTCCTACAGG----AAG
                                                                                                                                                                                                                                                                                                                                                                                32 AlaAspAspThrTyrThrGluSerTyrIleSerThrIleGlyValAspPheLysIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                      10 TATAAACTTGTGGTAGTTGGAGCTTGTGGCGTÄGGCAÄGÄGTGCCTTGACGATACAGCTA 69
                                       GCCATAAATAATACTAAATCATTTGAAGATATTCACCATTATAGAGAACAAATTAAAAGA 306
                                                                                                                                                                                        LysLysValValAspTyrThrThrAlaLysGluPheAlaAspSerLeuGlyIleProPhe
                                                           TyrAla---SerGluAsnValAsnLysLeuLeuValGlyAsnLysCysAspLeuThrThr
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US-09-820-003B-2 (1-173) x US-08-306-691B-15 (1-5775)
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US-08-306-691B-15
                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                  Alignment Scores:
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                                                                                                                                          Query Match:
                                                                                                                                                                                                                              Pred. No.:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY_AGENT INFORMATION:
NAME: MONACO, DANIEL A.
REGISTRATION UNBER: 30,480
REFERENCE/DOCKET NUMBER: 8321
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
THIETERS (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (215) 568-5549
TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: doubl
TOPOLOGY: linear
MOLECULE TYPE: DNA (9
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTIERNSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 5775 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C. STREET: Two Penn Center, Suite 1800 CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: Septem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 Lys 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 GAAATTCGAAAACATAAAGAAAAGATGAGCAAAGATGGTAAAAAAGAAGAAAAAAGAAGTCA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 GluIleLysLysArgMetGlyProGlyAlaThrAlaGlyGlyAlaGluLysSerAsnVal 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 ATTCAAACATCAGCAAAGACAAGACAGGGTGTTGATGATGCCCTTCTATACATTAGTTCGA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 LeuGluThrSerAlaLysAsnAlaThrAsnValGluGlnSerPheMetThrMetAlaAla 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 ---AGAACAGTAGACACAAAACAGGCTCAGGACTTAGCAAGAAGTTATGGAATTCCTTTT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 AAG 546
                12 PheLysLeuLeuIleGlyAspSerGlyValGlyLysSerCysLeuLeuLeuArgPhe 31 :::||||||::::::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (215)
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N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                                         DNA (genomic)
                                                                                                                                  3.34e-19
218.50
49.17%
30.39%
24.66%
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                                                                                                                                                                                   Length:
Matches:
Conservative:
                                                                                                                                       Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
PCT-US93-06251-29
Sequence 29, Application PC/TUS9306251
SEQUENCE 11 PERORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5775 has
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                     REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                NAME: DiGiglio, Frank REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 GluIleLysLysArgMetGlyProGlyAlaThrAlaGlyGlyAlaGluLysSerAsnVal 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                616 ATTGAAACATCAGCAAAGACAAGACAGGGTGTTGATGATGCCTTCTATACATTAGTTCGA 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               559 ---AGAACAGTAGACAAAAACAGGCTCAGGACTTAGCAAGAAGTTATGGAATTCCTTTT 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439 GCCATAAATAATACTAAATCATTTGAAGATATTCACCATTATAGAGAACAAATTAAAAGA 498
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                5775 base pairs
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WENTION: Trivalent Synthesis of Oligonucleotides Containing
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29:
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Patent No. 5962243;

Patent No. 5962243;

GENERAL INFORMATION:

APPLICANT: BROWN, MICHAEL S.

APPLICANT: GOLDSTEIN, JOSEPH L.

APPLICANT: REISS, YUVAL

APPLICANT: JAMES.
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; STRANDEDNESS: doub.
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (
PCT-US93-06251-29
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Best Local Similarity:
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                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                              TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION TITLE OF INVENTION: TRANSFERASE INHIBITORS
                        STREET:
                                      ADDRESSEE: ARNOLD, WHITE & DURKEE
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           HOUSTON
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TEXAS
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24.66%
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-820-003B-2 (1-173) x US-08-429-964-83 (1-574)
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Best Local Similarity:
Query Match:
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DAIL:
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: PARKER, DAVID L.
NAME: PARKER, DAVID L.
155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US/91/02650
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: UT TELECOMMUNICATION INFORMATION: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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No.::
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FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (713)
TELEX: 79-0924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION · NUMBER:
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247 GCCATAAATAATACTAAATCATTTGAAGATATTCACCATTATAGAGAACAAATTAAAAGA
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                                                                             CAAGTAGTAATTGATGGAGAAACCTGTCTCTTGGATATTCTCGACACAGCAGGTCAAGAG 186
                                                                                                                                                                                                                               ATTGACAATCATTTTGTGGACGAATATGATCCAACAATAGAGGATTCCTACAGG---AAG 126
                                                                                                                                                                                                                                                                     AlaAspAspThrTyrThrGluSerTyrIleSerThrIleGlyValAspPheLysIleArg
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AER: PCT/US/91/02650
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Matches:
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Alignment Scores: 2.24e-20 L. Score: 217.50 M. Score Similarity: 46.888 C.	INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 803 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: 11near IMMEDIATE SOURCE: LIBRARY: OVARTUT10 CLORE: 2703745 US-09-075-454-13	PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: 08/766,551 FILING DATE: DECEMBER 12, 1996 ATTORNEY/AGENT INFORMATION: NAME: CEITONE, MICHAEL C. REGISTRATION NUMBER: 39,132 REFERENCE/DOCKET NUMBER: PF-0168-1 TELECOMMUNICATION INFORMATION: TELEPONE: 650-845-4166 TELEPA: TELEPA:	ZIP: 94304 ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: WOR'D PERFECT 6.1/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/075,454 FILING DATE: Herewith CLASGIFFCATTON:	Cal SERV	AGATCCGACAA 495 Application US/09075 91580 RMATION:	Oy 80 TyralaSerGluAsnValAsnLysLeuLeuValGlyAsnLysCysAspLeuThrThr :::
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Hest Local Similarity: 26.79% Mismatches: 61 Usery Match: 24.55% Indels: 58 Usery Match: 24.55% Indels: 58 Usery Match: 58	Qy 170 yGlyCysCys Db 648 GAATTGTTGC	Qy 152 yAlaGluL : Db 588 TGACAGCA	Qy 132 rPheMetr : ::: Db 543 TGTTCTGC	Qy 112 pSerLeuG ::: Db 483 GACGTATG	ОУ 98 r Db 423 САСТЭСТЭ	Qy 78 pargTyra : 1 Db 363 GGATGCAG	Qy 65 Db 303 GTATGATG	Db 243 GGAGAGAT	50 183	Qy 30 gPhealaa Db 123 ACTTTGCA	Qy 12PheLy ::: Db 63 GCTTACAA	Qy 3 SerMetAs ::::::: Db 3 GCACTCTC	Best Local Similarity: Ouery Match: DB: US-09-820-003B-2 (1-17
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Search completed: June 22, 2003, 18:56:58 Job time: 70 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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-O_-Cgn2_1/USFTO_Spool/US09820003/runat_18062003_144130_13104/app_query.fasta_1.327
-OB-EST -OFMT-fastap -SUFFIX=p2n.rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human#0.cd1 -LIST=45
-DCGALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-2000000000
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-NO_MMAP -LARGEQUERY -NGE_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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ALIGNMENTS

AUTHORS	REFERENCE	SOURCE ORGANISM	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AL539022	
11,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 948)	human. Homo sapiens	EST.	AL539022.1 GI:12867866	prime, mRNA sequence. AL539022	LTI_FL013_FBrn1 Homo sapiens cDNA clone CS	AL539022 948 bp mrNA linear EST 16-FEB-2001	-	

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Contact: Genoscope
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                                                                      GluPheAlaAspSerLeuGlyIleProPheLeuGluThrSerAlaLysAsnAlaThrAsn
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                                                       GAATTTGCTGATTCCCTTGGAATTCCGTTTTTGGAAACCAGTGCTAAGAATGCAACGAAT
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Location/Qualifiers
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/dev_stage="pooled tissue from post conception
week, 24 week and 26 week)"
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Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
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national Institutes of Health, Mg
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Contact: Robert Strausberg, Ph.D.
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                                                   GlyValGlyLysSerCysLeuLeuLeuArgPheAlaAspAspThrTyrThrGluSerTyr
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IleSerThrIleGlyValAspPheLysIleArgThrIleGluLeuAspGlyLysThrIle
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                                                                                                                                                                                                                                                                                                                                             source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

a 196 c 246 g 248 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed);
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/clone_lib="NIH_MGC_120"
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/db_xref="taxon:9606"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov plate: ILIAM12185 row: a column: 23 High quality sequence stop: 597. Location/Qualifiers 11130 /organism="Homo sapiens" /clone="IMAGE:5520670" /clone="IMAGE:5520670" /clone="IMAGE:5520670" /clone=lib="NHILMGC_71" /lab_host="public plange-resistant)" /lab_host="public plange-resistant)" /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. "	NII-WGC http://mgc.nci.nih.gov/. RS NII-WGC http://mgc.nci.nih.gov/. RS NII-WGC http://mgc.nci.nih.gov/. RS NII-WGC http://mgc.nci.nih.gov/. RI Unpublished (1999) AL Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation	s , z	149 ThralaGlyGlyAlaGluLysSerAsnValLysIleGlnSerThrProValLysGlnSer 168		ASHVALLYSGINTrpLeuGInGluIleAspArgTyrAlaSerGluAshValAshLysLeu	61 LysLeuglnIle	297 ATCACCACATTGGTGTGGATTTCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATC 356
RESULT 4 BQ223273 BQ223273 LCCUS DEFINITION AGENCORT.7518264 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6066561 ACCESSION BQ223273 VERSION BQ223273 VERSION BQ223273 SOURCE ORGANISM Homo sapiens CRYWORDS CORGANISM ELWARYOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFFERENCE AUTHORS NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999)	Db 658 GTAGAACAGTCTTCATGACGATGACAGTGAGATTAAAAAGCGAATGGGTCCCGGAGCA 717 Qy 149 ThralaGlyGlyAlaGluLysSerAsnValLysIleGlnSerThrProValLysGlnSer 168		Db 358 AAGCTTCAAATATGGGACACAGCAGGCCAGGAAAGATTTCGAACAATCACCTCCAGTTAT 417 Qy 65	Db 178 ATGTCCAGCATGAATCCCGAATATTATTTATTCAAGTTACTTCTGATTGGCGACTCA 237 Qy 21 GlyValGlyLysSorCysLeuLeuLeuArgPheAlaAspAspThrTyrThrGluSerTyr 40	-09-820-	Alignment Scores: 5.4e-93 Length: 1130 Pred. No.: 5.4e-93 Length: 171 Score: 849.00 Matches: 171 Percent Similarity: 83.41% Conservative: 0 Best Local Similarity: 83.41% Mismatches: 2 Query Match: 95.82% Indels: 32 DB: 13 Gaps: 1	BASE COUNT 319 a 241 c 290 g 280 t ORIGIN

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Plate: LLAM13344 row: k column: 10
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/db_xref="taxon:9606"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution informatifound through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llni.gov
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National Institutes of Health, Mammalian
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1 (bases 1 to 944)
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                                            IleGlyValAspPheLysIleArgThrIleGluLeuAspGlyLysThrIleLysLeuGln
                                                                                                                                                                       AAGTCCTGCCTTCTCCTTAGGTTTGCAGATGATACGTATACGGAAAGCTACATCAGCACA
                                                                                                                                                                                                               LysSerCysLeuLeuArgPheAlaAspAspThrTyrThrGluSerTyrIleSerThr
                                                                                                                                                                                                                                                                                                                                               ATGAATCCCGAATATGATTATTTATTCAAGTTACTTCTGATTGGCGATTCTGGGGTTGGA
                                                                                                                                                                                                                                                                                                                                                                                       MetAsnProGluTyrAspTyrLeuPheLysLeuLeuLeuILeG1yAspSerG1yValG1y
    ATTGGTGTGGATTTCAAGATACGAACTATAGAGTTAGATGGGAAAACAATCAAGCTACAG
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NIH_MGC_12"
/clone_lib="NIH_MGC_12"
/lab_host="DH10B (phage-resistant)"
/note="Organ: olfactory epithelium; Vector:
/note="Organ: olfactory epithelium; Vector:
pcMV-SPORT6.l.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
pcMV-SPORT6.l.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
pcMV-SPORT6.l.ccdb; Site_1: Rock; Cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer: Oligonially. Oligonially. Primer: Oligonially. 
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/clone_lib="NIH_MGC_129"
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/db_xref="taxon:10090"
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Ls a NIH_MGC
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Rodentia;
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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clone IMAGE:6315467
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; Murinae; Mus
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172 CysCys 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AACAAATGTGACCTGACCACAAAGAAAGTAGTAGACTACACAACAGCAAAGGAATTTGCA 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 AsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLysGluPheAla 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             African clawed frog.

Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.

1 (bases 1 to 646)
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                                                                                                                                                                                                                                                                                                                                                                                                             Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed genes in X. laevis embryo Unpublished (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tadasu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
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                                                                                                                                                                                                                                                                                                                                                                                            81-559-81-6856
81-559-81-6855
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                                                    /tissue_type="whole embryo"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
/note="Yector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-d" primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
                                             (Wellcome/CRC Institute).
129 c 161 g 148
                                                                                                                                                                                                                                                          /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL141f18"
                                                                                                                                                                                                                                                                                                                           nini@genes.nig.ac.jp.
Location/Qualifiers
1..646
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                                                              REFERENCE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 TACAGGGGAGCCCACGGCATCATTGTTGTGTATGACGTAACAGACCAGGAATCCTTCAAC
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                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 957)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                          BQ219698 957 bp mRNA linear EST
AGENCOURT_7578277 NCI_CGAP_Stl Mus musculus cDNA clone
IMAGE:6051445 5', mRNA sequence.
                                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                            BQ219698.1 GI:20401098
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514

REFERENCE AUTHORS

COMMENT

TITLE JOURNAL

FEATURES

ORIGIN

BASE COUNT

SOURCE ORGANISM

밁 Q 밁 Ş 밁 Ş

620

560 152 500 132

274 64 214 154

94

DEFINITION BJ093078

ACCESSION EYWORDS ERSION

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Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                             LeuValGlyAsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLys
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GlyGlyGlyCysCys 173
                                ValGluGlnSerPheMetThrMetAlaAlaGluIleLysLysArgMetGlyProGlyAla
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                                                                                                                GTAGAACAGTCTTTCATGACGATGGCAGCTGAGATTANAAAGCGAATGGGTCCTGGAGCT
                                                                                                                                                                                             GAATTTGCAGATTCCCTTGGAATTCCATTTTTGGAAACCAGTGCTAAGAACGCAACGAAT
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Location/Qualifiers
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/Clone_lib="NCI_CGAP_St1"
/Clone_lib="NCI_CGAP_St1"
/lab_host="DH10B_(T1-resistant)"
/note="Organ: stomach; Vector: pcMV-SPORT6; Site_1: Sali, Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.77 kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP_Library."
a 208 c 250 g 229 t l others
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REFERENCE
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 864)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ437146 864 bp
AGENCOURT_7909781 NIH_MGC_71 Homo
5', mRNA sequence.
BQ437146
BQ437146.1 GI:21176210
EST.
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Plate: LLAM13500 row: e column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                               GlyValGlyLysSerCyśLeuLeuLeuArgPheAlaAspAspThrTyrThrGluSerTyr 40
                                                                                                                                                                                                                                                                              MetSerSerMetAsnProGluTyrAspTyrLeuPheLysLeuLeuLeuIleGlyAspSer
TACAGAGGAGCCCATGGCATCATAGTTGTGTATGATGATGACAGATCAGGAGTCCTTCAAT
                                                                                                LysLeuGlnIle--
                                                                                                                                 ATCAGCACAATTGGTGGATTTCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATC
                                                                                                                                              IleSerThrIleGlyValAspPheLySIleArgThrIleGluLeuAspGlyLysThrIle
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone=_TMAGE:6156281"
/clone_1ib="NIH_MGC_71"
/tissue_type="lelomyosarcoma"
/tissue_type="lelomyosarcoma"
/lab_host-"DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6
Site_2: SalI; Cloned unidirectionally. P
Average insert size 2.1 kb. "
a 171 c 231 g 213 t
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AGENCOURT_8858773 NCI_CGA
IMAGE:6441874 5', mRNA se
BQ944368
BQ944368.1 GI:22359846
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Eukaryota; Me
Mammalia; Eut
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://lnage.llnl.gov
plate: LLAM13965 row: m column: 11
High quality sequence stop: 662.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, w
Unpublished (1999)
Contact: Robert Strausberg, Ph.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases
                                                                                                 246
                                                                                                                                                                     /organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:6441874"
/clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                          /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

197 c 243 g 214 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 to 901)
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E 1 (bases 1 to 1165)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) (Inpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: AFCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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plate: LLAM12200 row: j
High quality sequence sto
                                                                       -GlyGlyGlyCysCys 173
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                                              ThrAlaGlyGlyAlaGluLysSerAsnValLysIleGlnSerThrProValLysGlnSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/db_xref="Taxon:9506"
/clone=_lib="NMAGE:5526635"
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/note="organ: skin; Vector: pcWV-SPORT6; Site_1: N
/note="stal; Cloned unddirectionally. Primer: Ol
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8 others
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Hegde, P., Q1.R., Abernathy, K.,
I.E., Saeed, A.I., Sharov, V., I
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Plate: 63
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The Institute for Genomic
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US-09-820-003B-2 (1-173) x AL530265 (1-945) QY 1 MetSerSerMetAsnProGluTyrAspTyrLeuDheLysLeuLeuIleGlyAspSer 20	Alignment Scores: Pred. No.: 809.00 Percent Similarity: 93.01% Best Local Similarity: 93.01% Conservative: 945 Matches: 171 Conservative: 9 Mismatches: 2 DB: 9 Gaps: 1	/or	urce S		RESULT 12 AL530265 AL530265 AL530265 LOCUS AL530265 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD009YH19 5 Pilme, mRNA sequence. ACCESSION AL530265 VERSION AL530265 VERSION AL530265 SURCE NUMBAN SEGUENCE SOURCE NUMBAN SADIens ADSANISM Homo sapiens	Qy 109 GluPheAlaAspSerLeuGlyTleProPheLeuGluThrSerAlaLysAsnAlaThrAsn 128 Db 451 GAATTTGCTGATTCCCTTGGAATTCCGTTTTTGGAAACCAGGGCTAAGAATGCAACGAAT 510 Qy 129 ValGluGLISerPheMetThrMetAlaAlaGLUTleLysYsArgMetGlyProGlyAla 148 Db 111111111111111111111111111111111111
source	COMMENT CONTRACT: TO CENTER FOR NATIONAL I 1111 Yatta, Tel: 81-55 Fax: 81-55 Fax: 81-55 Fatures	RESULT 13 BJ073109 LOCUS DEFINITION ACCESSION VERSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	Db 660 ACACCTCC Qy 169 -GlyGlyG	129 601 149	Oy 09 ASIN'ALLY Db 421 AATGTTAA O1 Oy 89 LeuValG1 Db 481 TTGGTAGG Oy 109 GluPheAl Db 541 GAATTTTGG	Db 181 Oy 41 Db 241 Oy 61 Oy 65 Db 361

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hini@genes.nig.ac.jp.
Location/Qualifiers
1. 642
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL108p01"
/clone="XL108p01"
/clone=1b="NIBB Mochii normalized Xenopus tailbud
                                                                                                                                                                                                                                                   or Genetic Resource Information
Institute of Genetics
, Mishima, Shizuoka 411-8540, Japan
159-81-6856
                                                                                                                                                                                                                                                                                                                                                               genes in X. laevis embryo ed (2001)
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
ae; Xenopus;
; 1 to 642)
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aevis
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NIBB Mochli normalized Xenopus tailbud library Xenopus
NA clone XL108p01 5', mRNA sequence.
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/tissue_type="whole embryo"
/dev_stage="stage 25"
                                                                                                                                                                                                                                                                                                                                            Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTCTTTCATGACGATGGCAGCTGAGATTAAAAAGCGAATGGGTCCGGA-GCA 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | InSerPheMetThrMetAlaAlaGluIleLysLysArgMetGlyProGlyAla 148
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 Eukaryota;
                     house mouse.
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          musculus
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                                                                                                                 612
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  Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.03e-88
808.50
81.68%
81.19%
91.25%
                                        GI:15647170
 Chordata;
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Vertebrata;
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Percent Similarity:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Tissue Procurement: Jeffrey Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                        MetSerSerMetAsnProGluTyrAspTyrLeuPheLysLeuLeuLeuIleGlyAspSer
sGluPheAlaAspSerLeuGlyIleProPheLeuGluThrSerAlaLysAsnAlaThrAs
                                                     uLeuValGlyAsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLy
                                                                                                           TAACGTTAAACAGTGGCTGCAGGAGATAGATCGCTACGCCAGTGAAAATGTCAACAAGTT
                                                                                                                               nAsnValLysGlnTrpLeuGlnGluIleAspArgTyrAlaSerGluAsnValAsnLysLe
                                                                                                                                                                                   TACAGAGGAGCCCCATGGCATCATAGTTGTGTATGATGTGACAGATCAGGAGTCCTTCAA
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                                    GTTGGTAGGGAACAAATGTGACCTGACCACAAAGAAAGTAGTAGACTACACAACAGCAAA
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone="ITMAGE:5343151"
/clone_lib="NCI_GAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating d
/dev_stage="5 months"
/lab_host="DH10B"
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1 0 h s c e e e e e e e e e e e e e e e e e e	6	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB: US-09-820-00	BASE COUNT	FEATURES SOURCE	ORGANISM ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 15 B1739625 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	8 1	, 1	6 1	0
	85 ATGTCCAGCATGAATACCGAATATGATTATTCAAGTTACTTCTGATTGGCGATTCTCT	timilarity: 82.21%	/Organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:5588676" /clone_lib="NIH_MGC_94" /tlssue_type="retina" /lab_host="DHIOB (phage-resistant)" /lab_host="DHIOB (pha	Tissue Procurement: The Cepko Laboratory CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11938 row: d column: 21 High quality sequence stop: 849. Location/Qualifiers 1.855	Motazoa; Chordata; Craniata; Vertebrata; Euteleostc utheria; Rodentia; Sciurognathi; Muridae; Murinae; to 855) p://mgc.nci.nih.gov/. stitutes of Health, Mammalian Gene Collection (MGC) (1999)	855 bp mRNA linear EST 20-SEP- NIH_MGC_94 Mus musculus cDNA clone IMAGE:5368676 57 ce . GI:15716638	68 SerGlyGlyGlyCys 	laThrAlaGlyGlyAlaGluLys-SerAsnValLysIleGlnSerThrProValLysGln 	128 nValGluGlnSerPheMetThrMetAlaAlaGluIleLysLysArgMet-GlyProGlyA 148 	

DЬ	Qy	Ф	Qy	Дb	Qy	Φ	Qy	рь	Qy	Ф	γO	Ф	γQ	Db	Qy	Ф	Qy	Дb
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SUMMARIES

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-QrGp2_1/USPF0_Sppol/US99820003/runat_18062003_144129_13082/app_guery.fasta_1.327
-QrGp2_1/USPF0_Sppol/US99820003/runat_18062003_144129_13082/app_guery.fasta_1.327
-DB=N Geneseq_101002 -QFMT=fastap -SUFFIX=P2n.xng -MINMATCH=0.1 -LOOPCIA-0
-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANSIN-human40.cd1
-LIST=45 -DCCALIGNE-200 -THR_SCORED=PCT -THR_MAX=100 -THR_MIN-0 -ALIGN=15
-MODE-LOCAL -OUTFMT=Pto -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09820003 =GCGN_1_396 &TUNAT_1805003 144129_13082 -NCUFG-6 -ICFU-3
-NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -TGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening
                                                                                                                                No.:
                                                                                                                                                                                    Sequence 723
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                                                                                                                                                               Human; secreted protein; diagnosis; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; notificalmmatory; antilicer; vulnerary; anticonvulsant;
                                                                                                                Ното
                   26-MAR-1999;
17-DEC-1999;
                                                                      05-OCT-2000
                                                                                            WO200058356-A1
                                                                                                                                                                                                            Human secreted
                                                                                                                                                                                                                                                     AAC60009;
                                                   22-MAR-2000; 2000WO-US07535
                                                                                                                                    neurological disease;
                                                                                                                                                         antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                           ValGluGlnSerPheMetThrMetAlaAlaGluIleLysLysArgMetGlyProGlyAla
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCAGCACAATTGGTGTGGATTTCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                GGTGGAGGTTGCTGC
                                                                                                                                                                                                                                                                                                                                                         ACAGCTGGTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysLeuGlnIle-----
                                                                                                                                                                                                                               (first entry)
                                                                                                                                               antifungal; antiparasitic; cardiant; gene therap;
disorder; cardiovascular disorder; wound healing
                   990S-0126511.
990S-0172413.
                                                                                                                                                                                                            protein gene 44 SEQ ID NO:54.
                                                                                                                                                                                                                                                                        CDNA;
                                                                                                                                     infectious
                                                                                                                                                       gene therapy;
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(HUMA-) HUMAN

GENOME SCI INC

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-820-003B-2 (1-173) x AAC60009
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                                                                                                                                                                  AAGCTTCAAATATGGGACACAGCAGGCCAGGAAAGATTTCGAACAATCACCTCCAGTTAT
                                                                                                                                                                                                                                                                                LysLeuGlnIle----
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LeuValGlyAsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLys
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This sequence encodes a human Rab protein of the invention, designated CC RABP-2. The Rab proteins, RABP-1, RABP-2 and RABP-3 are involved in CC vesicle trafficking, cell function, and cell differentiation. The RABP CC polypeptides, DNAs and agonists can be used to prevent or treat a consider associated with an increase in appotosis, e.g. infectious or CC genetic immunodeficiencies, neurodegenerative diseases such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, cretinitis pigmentosa, and cerebellar degeneration, myelodysplastic cretinitis pigmentosa, and cerebellar degeneration, myelodysplastic Syndromes such as aplastic anemia, ischaemic injuries such as wyocardial infarction, stroke, and reperfusion injury, toxin-induced diseases such as a cachexia, viral infections, and osteoporosis. They can consist such as cachexia, viral infections, and osteoporosis. They can consist to fight an infection or a cancer or to correct a correct and consist or Huntington's chorea. Antagonists can be used to prevent or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified human Rab proteins - used to develop products for treating e.g. AIDS, immunodeficiencies, neurodegenerative diseases, cancer, inflammation or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rab protein; RABP-1; RABP-2; RABP-3; human; vesicle trafficking; cance; cell differentiation; apoptosis; immunodeficiency; cell proliferation; neurodegenerative disease; myelodysplastic syndrome; wasting disease; toxin-induced disease; infection; genetic defect; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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DB; AAY00919.
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AAF21661;
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US-09-820-003B-2 (1-173) x AAF21661
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                                                                                                                                                                                                                       antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; anticonvulsant; anticonvulsant; anticonvulsant; anticonvulsant; The antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, allergies, autoimmune colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as
                                                                                                                                                                                                                                                                                                                                                                                          Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; noutropic; neuroprotective; antiviral; antiallergic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nootropic; neurpprotective; antiviral; antiallergic; hepatotro antidiabetic; antiinflammatory; antiolicer; vulnerary; anticom antibacterial; antifungal; antiparasitic; cardiant; immune dia Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; muntiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease;
                                                                                                                                                                          Sequence 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                          anoxia
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ntiviral; antiallergi
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   07-MAR-2000;
19-MAY-2000;
17-JUN-2000;
14-JUL-2000;
                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; arthritis; Crohn's disease; sepsis; shock; ischaemia-reperfusion injury; haematopolesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; peridontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen; ss.
                                                                                                                                05-MAR-2001;
                                                                                                                                                                                       13-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding novel human secretory protein, Seq ID
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The invention relates to novel isolated human secreted polypeptides (I) cand polynucleotides (II). (I) and (II) are useful for treating the financiary conditions such as arthritis, nephritis. Croin's disease, considered in increasing haematopolesis, stemure responses, and is converted in increasing haematopolesis, stem cell survival, bone growth converted in increasing haematopolesis, stem cell survival, bone growth converted in increasing haematopolesis, stem cell survival, bone growth converted in increasing haematopolesis, stem cell survival, bone growth converted in increasing haematopolesis, stem cell survival, bone growth converted in increasing haematopolesis, stem cell survival, bone growth converted in the polypeptides of the polypeptides of the polypeptides of the polypeptides of the polypeptides. Converted in the polypeptides in the polypeptides in a train this sue and is useful for studying modulators of the polypeptides. Converted in induces the proliferation of neural cells and regeneration of nerve converted in the polypeptides. Converted in the polypeptides in the polypeptides in the polypeptides in the polypeptides. In addition, (I) is involved in chemotactic or chemokinetic converted in the polypeptides in the polypeptides in the polypeptides. Converted in the polypeptides in the polypeptides in the polypeptides in the polypeptides. Converted in the polypeptides in the polypeptides in the polypeptides in the polypeptides. In addition, (I) is also useful for treating mysloid converted in the polypeptides in the polypeptides. In addition, the polypeptides in the polypeptides. In addition, the polypeptides in the polypeptides in the polypeptides. In addition, the polypeptides of the polypeptides in the polypeptides. In addition, the polypeptides in the polypeptides in the polypeptides in the polypeptides. In addition, (I) is also useful for treatment of lung or liver fibrosis, the polypeptides in the polypeptides in the polypeptides in the polypeptides in the polypeptides. In addition, (I) affect
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P-PSDB; AAU28024.
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Zhang J, Chen
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SerThrIleGlyValAspPheLysIleArgThrIleGluLeuAspGlyLysThrIleLys
                                 GTGGGCAAGTCATGCCTGCTGCGGTTTGCTGATGACACGTACACAGAGAGCTACATC
                                             ValGlyLysSerCysLeuLeuArgPheAlaAspAspThrTyrThrGluSerTyrIle
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          Claim 1;
                          Isolated nucleic acids diagnosing and treating disorders -
                                                          WPI; 2001-514838/56
P-PSDB; AAO13525.
                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                   28-FEB-2000;
18-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                      The invention relates to novel nucleic acids encoding novel human foetal CC antigens. The nucleic acids and proteins are used to prevent, treat (e.g. by gene therapy) or ameliorate a medical condition in e.g. humans, mice, CC by gene therapy) or ameliorate a medical condition in e.g. humans, mice, CC rabbits, yoats, horses, cats, dogs, chickens or sheep. They cC are also used in diagnosing a pathological condition or susceptibility CC to a pathological condition. The antibodies to the antigens can also be used in alleviating symptoms associated with the disorders and in CC immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis.

CC cardiovascular disorders e.g. neoplasms of the breast or liver, CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, provides and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to regenerate tissues and in chemotaxis. The polypeptides can also be used to subditive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, contents and other nutritional components. Numerous
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17-NOV-2000;
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01-DEC-2000;
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                                                                                                                                                                                                                                     examples of diseases and disorders treated by the nucleic acids and proteins are given in the specification. The present sequence is a genomic DNA fragment from a gene encoding a foetal antigen of
                                                                                                                                                                                                   No : :
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73.53%
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New isolated nucleic genes from Drosophila interactions
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11-JUL-2000;
                                                                                                                                                                                                                23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                       pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental
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DB; ABB61880.
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                                                                                                                                                                                                                                                                                                                                                                                   melanogaster expressed polynucleotide SEQ ID NO 12431
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2000US-0614150
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              detection reagent for detecting for elucidating cell signalling
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US-09-820-003B-2 (1-173) x ABL05983 (1-1791)
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                                                   AAF14053 standard; cDNA; 1202
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AAF14053;
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                                                                                                                                                                                                                 SerGlyGlyGlyCysCys 173
                                                                                                                                                                                                                                                                        AGCGCCACTGAC --- PACGCTAGCAAAGTGAAAATCGATCAAGGACGTCCAGTGGAAAAC
                                                                                                                                                                                                                                                                                                                           ThrAlaGlyGlyAlaGluLysSerAsnValLysIle---GlnSerThrProValLysGln 167
                                                                                                                                                                                                                                                                                                                                                                                  GTTGAGCAGGCCTTCATGACGATGGCGGCGGAGATCAAGAATCGCGTCGGGCCGCCGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                              No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 88; Page 2691; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monitoring differential expression of genes in filamentous fungal celuses fluorescence-labeled nucleic acids isolated from the cells and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.
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                                                                                                                                                                                  Sequence 1202 BP; 282 A; 294 C; 282 G; 344 T; 0 other;
                                                                                                                                                                                                                                all specifically claimed in the present invention.
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                      GluGlnSerPheMetThrMetAlaAlaGluIleLysLysArgMetGlyProGlyAlaThr
                                                                                                                      AGAGGAGCTCATGGAATTATTGTGACTTATGATGTAACAGATCTAGAAAGCTTCAACAAC
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              GAAGAAGCTTTCATGGCCATGACTCCTGCAATCAAGACCAGAATGGCG---AGCCAACCT
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KW Human; chromosome mapping; gene map KW food supplement; medical imaging; d XX
KW Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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                                                          ThrSerAlaLysAsnAlaThrAsnValGluGlnSerPheMetThrMetAlaAlaGluIle
                                                                                                                                   ValValAspTyrThrThrAlaLysGluPheAlaAspSerLeuGlyIleProPheLeuGlu
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Percent Similarity: Best Local Similari Query Match:

Similarity:

1.9e-61 619.50 68.97% 61.58% 69.92%

Conservative: Mismatches: Indels:

Length: Matches:

Pred. No.: Alignment

at seqdata.uspto.gov/sequence.html?DocID=999909770445

BP;

241 A; 199

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other;

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CC comprising a sequence capable of hybridising under stringent conditions (1) of sequence selected from any one of 999 sequences (ABN98233-ABN99231), CC given in the specification or its fragment. A polypeptide (II) encoded by CC (I), a transgenic plant (III) comprising an exogenous nucleic acid, is CC useful for screening a candidate agent for its biological effect. (I) is CC useful in identifying homologous or related genes, in producing compositions that modulate the expression or function of its encoded protein, mapping functional regions of the protein and in studying are best capable of withstanding a particular disease or environmental cc stress. (II) and (III) are useful for screening of the protein and in studying crops to prevent or treat disease. (II) are also useful in screening assays of various plant strains to determine the strains that crops to prevent or treat disease. (II) are also useful in screening crops to prevent or treat disease. (II) are also useful in screening crops to prevent or treat disease. (II) are also useful in screening crops to prevent or treat disease. (II) are also useful in screening crops to proteins of interest, for enhance the action of tolerance cc expression of proteins of interest. (II) are also useful in screening crops to proteins of interest, for establishing the extent to which cc any specific insect and/or pathogen is responsible for damage to a particular plant, for identifying other mediators that enhance or induce tolerance to environmental stress. (I) is also useful convolved in a cc particular plant, for identifying other mediators that enhance or induce tolerance to environmental stress in of seathlishing the extent to which caps to the plant. (II) is useful in the study of genetic function and regulation, of the convolved in the study of genetic function and regulation.

CC for identifying productions of nutritional, commercial or medicinal value and convolved in the study of genetic function and regulation.

CC for interation but was obtained in electro
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Hurban
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GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
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LEDFORD B L.
WOESSNER J P.
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SUMMARIES

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Yamaguchi, K., Uchida, K., Takai, Y., Aisaka, K. and S LOW-MOLECULAR WEIGHT PROTEIN BINDING TO GUANOSINE Patent; JP 1992226000-A 3 14-AUG-1992;
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SAKURADA KAZUHIRO
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25-APR-1991 JP 1991095304
21-MAY-1990 JP 90P 130547
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AF498929.
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Puhl, H.L. III, Ikeda, S.R. and
Homo sapiens RAB family small
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                  /product="small GTP binding protein RAB1A"
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odb_xref="taxon:9606"
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301 AATGTTAAACAGTGGCTGCAGGAAATAGATCGTTATGCCAGTGAAAATGTCAACAAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 723)

Eabhraoui, A., Touchot, N., Chardin, P. and Tavitian, A.

The human Rab genes encode a family of GTP-binding proteins related to yeast rpr1 and SEC4 products involved in secretion

J. Biol. Chem. 264 (21), 12394-12401 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMRABIA 723 bp mrNA linear PRI 08-JAN-1995 HOMO Sapiens GTP-binding protein (RABI) mRNA, complete cds. M28209 J04941 M28209.1 GI:550059 GTP-binding protein; ras oncogene. Homo sapiens (tissue library: of J.Mallet) pheochromocytoma cDNA to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValGluGlnSerPheMetThrMetAlaAlaGluIleLysLysArgMetGlyProGlyAla 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGCTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCA 600
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                                                                                                                                                                                                                                                                                                                                        27, 1994 this sequence version Location/Qualifiers
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/tissue_lib="of J.Mallet"
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                                                                                                                                                                                                                                                                                                                                                                                591 ACAGCTGGTGCTGAGAAGTCCAATGTTAAAATTCAGAGCACTCCAGTCAAGCAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                         149 ThrAlaGlyGlyAlaGluLysSerAsnValLysIleGlnSerThrProValLysGlnSer 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   531 GTAGAACAGTCTTTCATGACGATGGCAGCTGAGATTAAAAAGCGAATGGGTCCCGGAGCA
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Canis familiaris
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 840)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 ATCAGCACAATTGGTGGGATTTCAAAATAAGAACTATAGAGTTAGACGGGAAAACAATC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 GGGGTTGGAAAGTCTTGCCTTCTTAGGTTTGCAGATGATACATATACAGAAAGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 TACAGAGGAGCCCATGGCATCATAGTTGTGTATGATGTGACAGATCAGGAGTCCTTCAAT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 ATGTCCAGCATGAATCCCCGAATATGATTATTTATTCAAGTTACTTCTGATTGGCGACTCA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LysLeuGlnIle----- 64
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                                                                                                                                                                 Canine rabl mRNA for ras-related GTP-binding protein involved in membrane traffic.
                                                                                   GTP-binding protein; protein transport; Canie familiaris.
                                                                                                                             X56384.1 GI:913
                                                                                                                                                                                                                   CFRAB1
                                                                                                                                                                                                                                                                                                                            GlyGlyGlyCysCys 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | IleSerThrIleGlyValAspPheLysIleArgThrIleGluLeuAspGlyLysThrIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAATTTGCTGATTCCCTTGGAATTCCGTTTTTGGAAACCAGTGCTAAGAATGCAACGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluPheAlaAspSerLeuGlyIleProPheLeuGluThrSerAlaLysAsnAlaThrAsn 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuValGlyAsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLys 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGCTTCAAATATGGGACACAGCAGGCCAGGAAAGATTTCGAACAATCACCTCCAGTTAT 290
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KQWIQBIDRYASENVNKLLVGNKCDLTIKKVVDYTTAKEFADSLGIPFLETSAKNATN
VEQSEMTWAAEIKKRWGPGATAGGAEKSNVKIQSTPVKQSGGCC"
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                 Chordata; Craniata; Vertebrata; Euteleostomi; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 840)
Zerial, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-AUG-1990) Zerial Heidelberg, FRG
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                                          TTGGTAGGGAACAATGCGATCTGACCACAAAGAAAGTAGTAGACTACACAACAGCAAAG
                                                           LeuValGlyAsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLys
                                                                                                   AATGTTAAACAGTGGCTGCAGGAAATAGACCGTTATGCCAGTGAAAACGTCAACAAGTTG
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GVDFK.IRTIELDGKTIKLQIMDTAGQERFRTITSSYYRGAHGIIVYZDVTDQESFNNV
KQMLQEIDRYASENVNKLLVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATN
VEQSFWTMAAEIKKRMGFGATAGGAEKSNVKIQSTPVKQSGGGCC"

176 c 220 g 194 t
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/strain="cocker spaniel"
/db_xref="taxon:9615"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAB56775.1"
/db_xref="GI:6006435"
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KEYWORDS
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Y00094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haubruck,H., Disela,C., Wagner,P. and Gallwitz,D. The ras-related ypt1 protein is an ubiquitous euk isolation and sequence analysis of mouse cDNA clc homologous to the yeast YPT1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-NOV-1987) Gallwitz D., Max-Planck-Institut fuer biophysikalische Chemie, Abt. Molekulare Genetik, Postfach 28 D-3400 Goettigen, FRG 2 (bases 1 to 1428)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ras-related protein;
Mus musculus.
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1428
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263 c 324 g
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                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
on Jul 12, 2001 this sequence version replaced gi:12654174.
Contact: MGC help desk
mail: egapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hul
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BC000905.2 GI:14705268
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   Hale, S.M., Hulyk,
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                                                            109 GluPheAlaAspSerLeuGlyTleProPhcLeuGlvThrSerAlaLsysAsnAlaThrAsn 128 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4886442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IleSerThrIleGlyValAspPheLysIleArgThrIleGluLeuAspGlyLysThrIle 60
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GYDFKIRTIELDGKTIKLQIMDTAGQERFRTITSSYYRGAHGIIVYYDYTDQESFUNV
KQWLQEIDRYASENVIKLLYGNKÖDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATN
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/db_xref="Locus 10:5861"
/db_xref="Laxon:9606"
/clone="MGC:5233 IMAGE:2900705"
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/product="RAB1, member RAS oncogene family"
/prottein_i0="AAH00905.1"
/db_xref="GI:12654175"
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/clone_lib="NIH_MGC_10"
/lab_host="DH10B"
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IMAGE:3592802, mRNA, comp
BC002077
BC002077.1 GI:12805232
MGC
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NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (31-JaN-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution informat
through the I.M.A.G.E. Consortium/LLNL at: http://i
Series: IRAK Plate: 11 Row: a Column: 2
This clone was selected for full length sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene Collection (MGC), Cancer Ger Institute, 31 Center Drive, Room
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg, R.
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Mammalia; Eutheria;
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                                                                                                                                                                                                /clone="MGC:6226 IMAGE:3592802"
/tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Mam1"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
196. .813
                                                             /translation="MSSMNPEXDYLFKLILICDSGVGKSCLILFRADDTYTESYISTI
GVDFKIRTIELDGKTIKLQIWDTAGQERERTIISSYYRGALIVVYDVTDQESENNV
KQWLQBIDRYASENVNKLLVGNKCDLTTKKVVDYTTAKEFADSLGIPFLETSAKNATN
VEQSFMTMAAEIKKRMGPGATAGGAEKSNVKIQSTPVKQSGGGCC"
                                                                                                                    /product="RAB1, member RAS
/protein_id="AAH02077.1"
/db_xref="GI:12805233"
/db_xref="LocusID:5861"
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford
M., Schmutz, J., Grimwood, J., Rodr
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Direct Submission
Submitted (19-JAN-2000) :
Cincinnati, 231 Bethesda
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AF226873
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                                                                         Unpublished
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G. and Dorn, G.W.
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Medicine, University of Cincinnati, OH 45267-0590,
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                                     629 GGTGGAGGCTGCTGC 643
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                                                                                                                                                   129 ValGluGlnSerPheMetThrMetAlaAlaGluIleLysLysArgMetGlyProGlyAla 148
                                                                                                                                                                                          449 GAATTTGCAGATTCCCTTGGAATTCCATTTTTGGAAACCAGTGCTAAGAACGCAACGAAT 508
                                                                                                                                                                                                                                            389 TTGGTAGGGAACAAATGTGACCTGACCACAAAGAAAGTAGTAGACTACACAACAGCAAAG
                                                                                                                                                                                                                                                                                            329 AACGTTAAACAGTGGCTGCAGGAGATAGATCGCTACGCCAGTGAAAATGTCAACAAGTTG
                                                                                                                                                                                                                                                                                                                                               269 TACAGAGGAGCCCATGGCATCATAGTTGTGTATGATGTGACAGATCAGGAGTCCTTCAAT
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                                                                                                                                                                                                                                                                                                            69 AsnValLysGlnTrpLeuGlnGluIleAspArgTyrAlaSerGluAsnValAsnLysLeu 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"small GTP-binding protein RABIA"
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VEOSFMTMAAEIKKRHGPGATAGGAEKSNVKIQSTPVKQSGGGCC"
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/db_xref="taxon:10090"
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301 AACGTGAAACAGTGGCTGCAGGAGATCGATCGCTACGCCAGCGAAAATGTCAACAAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ATCAGCACGATTGGTGGATTTCAAGATACGGACTATAGAGCTAGACGGGAAAACAATC 180
                                  89 LeuValGlyAsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLys 108
                                                                                                                                                                      69 AsnValLysGlnTrpLeuGlnGluIleAspArgTyrAlaSerGluAsnValAsnLysLeu
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
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Proc. Natl. Acad. Sci. U.S.A. 84 (23), 8210-8214 (1987)
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TTGGTAGGGAACAAATGTGACCTGACCACAAAGAAAGTAGTAGACTACACAACAGCCAAG
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VEQSEMTMAABIKKRWGPGATAGGAEKSNVKIQSTPVKQSGGGCC"
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Draft entry and computer-readable
by J.K.Ngsee, 10-SEP-1990.
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1 (bases 1 to 841)
Ngsee,J.K., Elferink,L.A. and Scheller,R.H.
A family of ras-like GTP-binding proteins ex
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Stanford, CA 94305-5020
Stanford, CA 94305-5020
Aft entry and computer-readable
J.K.Ngsee, 10-SEP-1990.
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                                                                             /Product="GTP-binding protein"
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AFMTMAAEIKKRMGPGATSGGSEKSNVNIQSTPVKSSGGGCC"

154 c 194 g 224 t
                                                                                                                                                               /gene="o-rab1"
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                                                                                                                                                                                                               /organism-"Discopyge ommata"
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/tissue_type-"electric lobe"
                                                                                                                                                                                                              'tissue_type="electric
  9.05e-73
838.00
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130 GGTGTTGGAAAATCTTGTCTCCTCCTTAGATTTGCAGATGATACATATACAGAAAGTTAT
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Sequence 4 from patent US
AR070365
AR070365.1 GI:7221253
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Hillman, J.L., Lal, P.,
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AX086155 LOCUS AX086155 LOCUS AX086155 LOCUS ACCESSION AX086155 ACCESSION AX086155 EXETMORDS SOURCE ORGANISM HOMO saplens ORGANISM ATTILE AUTHORS JOURNAL FEATOURS FORMAL EACH COMMAN LOCATION ACCESSION AX086155.1 GI:13275888 ENERGYORDS LOCATION AX086155 ENABLES SOURCE AUTHORS AUTHORS AUTHORS FEATORES LOCATION EASE COUNT ORIGIN BASE COUNT A12659 LOCATION ACCESSION AX086155 GRIGIN ANDRIAL BASE COUNT AX086155 I GI:13275888 LOCATION PATENTIA: EVETEBRATE LOCATION PATENTIAL EVETEBRATION: LOCATION ALIGN ALIGN ALIGN ANDRIAL FORMAL LOCATION ALIGN ALIGN ALIGN ANDRIAL FORMAL LOCATION ALIGN ALIGN ALIGN ANDRIAL FORMAL LOCATION ALIGN ALIGN ALIGN ALIGN ALIGN ALIGN ALIGN ALIGN ANDRIAL FORMAL LOCATION ALIGN ALIG	Db 600 TCTGGGGGCGAGCGGCCCAATCTCAAGATCGACAGCACCCCTGTAAAGCCGGCTGGC 656 Qy 170 GlyGlyCysCys 173	Ph TT	300 CGGGGGCTCATGGCATCATCGTGGTGTATGACGTCACTGACCAGAATCCTACGCCAAC 70 VallysGlnTrpLeuGlnGluIleAspATgTyTAlaSerGluAsnValAsnLysLeuLeu 111111111111111111111111111111111	Qy 42 SerThIIIeGlyValAspPheLysIleArgThrIIeGluLeuAspGlyLysThrIIeLys 61	Query Match: 86.74% Indels: 33 DB: 6 Gaps: 2 US-09-820-003B-2 (1-173) x AR070365 (1-925) 2 SerSerMetAsnProGluTyrAspTyrLeuPheLysLeuLeuLeuIleGlyAspSerGly 21 Qy 2::::::!
Qy 170 GlyClycysCys 173 Db 639 GGTGCCTGTTGC 650 RESULT 13 HSM801608 LCCUS LCCUS DEFINITION Homo sapiens mRNA; cDNA DKFZp5641172 (from clone DKFZp5641172); ACCESSION AL136635 VERSION AL136635.1 GI:12052795 KEYWORDS SOURCE ORGANISM Homo sapiens ELMaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1985) AUTHORS Widemann, S. TITLE JOURNAL Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERMANY COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;			222 CTTCAGATCTGGGACACAGCGGGCCAGGAACGGTTCCGGACCATCACTTCCAGCTACTAC 65	Qy 22 ValGlyLysSerCysLeuLeuArgPheAlaAspAspThrTyrThrGluSerTyrIle 41	Pred. No.: 1.46e-65 Length: 1985 Score: 768.50 Matches: 156 Percent Similarity: 80.39% Conservative: 8 Best Local Similarity: 76.47% Mismatches: 7 Query Match: 86.74% Indels: 3 DB: 6 Gaps: 2 US-09-820-003B-2 (1-173) x AXO86155 (1-1985) Qy 2 SerSerMetAsnProGluTyrAspTyrLeuPheLysLeuLeuLeuLeulleGlyAspSerGly 21 ::::::

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BASE COUNT
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This clone (DKFZp5641172) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available
                                                                                                                                                                                                                                                                                                                                                            ValGlyLysSerCysLeuLeuLeuArgPheAlaAspAspThrTyrThrGluSerTyrIle
                                                          ValLysGlnTrpLeuGlnGluIleAspArgTyrAlaSerGluAsnValAsnLysLeuLeu
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ValGlyAsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLysGlu
                                                                                                               CGGGGGGCTCATGCCATCATCGTGTGTATGACGTCACTGACCAGGAATCCTACGCCAAC
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                                      GTGAAGCAGTGGCTGCAGGAGATTGACCGCTATGCCAGCGAGAACGTCAATAAGCTCCTG
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48. .653
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/tissue_type="brain"
/clone_lib="564 (synonym: hfbr2). Vector pAMP1;
X1-2blue; sites NotI + SalI"
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LQEIDRYASENYNKLLYGNKSDLTYKKYYDNTTAKEFADSLCIPFLETSAKNATNYEQ
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/protein_id="CAB66570.:
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/db_xref="taxon:9606"
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Rattus sp.
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X13905
X13905.1 GI:57005
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                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 654)
Vielh, E., Touchot, N
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Mammalia; Eutheria;
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12. .617
                                                                                                                                                                                       /protein_id="CAA32105.1"
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Rodentia;
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Murinae;
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Muzny, D. M., Adams, C., Adio-Oduola, B., All-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbarla, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bunder, G., Burch, P., Burkett, C., Burcell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falla, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Gadis, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 ValGlyAsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLysGlu 109
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366 GTAGGCAACAAGAGTGACCTCACCACCAAGAAGGTCGTGGACAATACCACAGCCAAGGAA 425
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCACCATTGGGGTGGACTTCAAGATTCGAACCATTGAACTGGATGGCAAAACCATCAAA 185
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Direct Submission
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Center project name: GRY0
Center clone name: CH20-117N16
Center clone name: CH20-117N16
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 102133 bases at least 030
Consensus quality: 108299 bases at least 030
Consensus quality: 114299 bases at least 020
                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                  as soon as it
be preserved.
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1108: contig of 1108 bp in le
1208: gap of unknown length
2485: contig of 1277 bp in le
2585: gap of unknown length
3731: contig of 1146 bp in le
3831: gap of unknown length
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GluGlnSerPheMetThrMetAlaAlaGluIleLysLysArgMetGlyProGlyAlaThr
                                                                       PheAlaAspSerLeuGlyIleProPheLeuGluThrSerAlaLysAsnAlaThrAsnVal
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                                                       TTTGCAGACTCTCTGGGTGTCCCCTTCCTGGAGACAAGTGCCAAGAATGCCCACCAATGTT
                                                                                                                                               ValGlyAsnLysCysAspLeuThrThrLysLysValValAspTyrThrThrAlaLysGlu
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                                                                                                                            GTAGGCAACAAGAGTGACCTCACCACCAAGAAGGTCGTGGACAATACCACAGCCAAGGAA
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